

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 5, 2004, 17:24:21 ; Search time 60 Seconds
(without alignments)
3583.644 Million cell updates/sec

Title: US-10-015-391A-277
Perfect score: 4031
Sequence: 1 MALPALGLDPWSLLGLFLFQ.....CRTSASDVADANNCLGTEVA 761

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	4031	100.0	761	3	AAy99418	Aay99418 Human PRO
2	4031	100.0	761	3	AAB24084	Aab24084 Human PRO
3	4031	100.0	761	4	AAB66167	Aab66167 Protein o
4	4031	100.0	761	4	AAM80295	Aam80295 Human pro
5	4031	100.0	761	4	AAB66043	Aab66043 Human TAN
6	4031	100.0	761	6	ABg72615	Abg72615 Human cyt
7	4031	100.0	761	6	ABU08366	Abu08366 Amino aci
8	4031	100.0	761	6	ABO32703	Abo32703 Secreted
9	4031	100.0	761	6	ABO33660	Abo33660 Novel hum

10	4031	100.0	761	7	ABO44513	Abo44513	Human	sec
11	4031	100.0	761	7	ABO33537	Abo33537	Novel	hum
12	4031	100.0	761	7	ADC18146	Adc18146	Human	PRO
13	4031	100.0	761	7	ADD70792	Add70792	Human	sec
14	4031	100.0	761	7	ADD39869	Add39869	Human	sec
15	4031	100.0	761	7	ADD70315	Add70315	Human	sec
16	4031	100.0	761	7	ADD38436	Add38436	Human	sec
17	4031	100.0	761	7	ADD39392	Add39392	Human	sec
18	4031	100.0	761	7	ADD38915	Add38915	Human	sec
19	4031	100.0	761	7	ADD40346	Add40346	Human	sec
20	4031	100.0	761	7	ADE50567	Ade50567	Human	sec
21	4031	100.0	761	7	ADE20179	Ade20179	Human	sec
22	4031	100.0	761	7	ADE50090	Ade50090	Human	sec
23	4031	100.0	761	7	ADE21648	Ade21648	Human	sec
24	3997	99.2	754	5	AAE18211	Aae18211	Human	MOL
25	3997	99.2	754	7	ADD18200	Add18200	Human	mol
26	3980	98.7	762	3	AAB37984	Aab37984	Human	sec
27	3966.5	98.4	756	5	AAE18210	Aae18210	Human	MOL
28	3966.5	98.4	756	7	ADD18198	Add18198	Human	mol
29	3875	96.1	730	4	AAB66045	Aab66045	Human	TAN
30	3875	96.1	730	6	ABO32705	Abo32705	Secreted	
31	3847.5	95.4	730	5	ABG79635	Abg79635	Human	nov
32	3821.5	94.8	728	6	ABR43294	Abr43294	Human	neu
33	3810.5	94.5	762	7	ADD67571	Add67571	Human	Ly6
34	3486	86.5	652	4	AAB66046	Aab66046	Human	TAN
35	3486	86.5	652	6	ABO32706	Abo32706	Secreted	
36	3333.5	82.7	631	6	ABR43277	Abr43277	Human	neu
37	3300.5	81.9	629	7	ADB64135	Adb64135	Human	pro
38	3280.5	81.4	760	4	AAB66084	Aab66084	Murine	se
39	3280.5	81.4	760	4	AAB66087	Aab66087	Murine	pr
40	3280.5	81.4	760	6	ABO32740	Abo32740	Secreted	
41	3280.5	81.4	760	6	ABO32738	Abo32738	Secreted	
42	1757.5	43.6	373	4	AAM80301	Aam80301	Human	pro
43	1743	43.2	328	4	AAB93948	Aab93948	Human	pro
44	1739	43.1	328	5	ABG66696	Abg66696	Human	nov
45	1274	31.6	837	3	AAY99410	Aay99410	Human	PRO

ALIGNMENTS

RESULT 1

AAY99418

ID AAY99418 standard; protein; 761 AA.

XX

AC AAY99418;

XX

DT 08-AUG-2000 (first entry)

XX

DE Human PRO1317 (UNQ783) amino acid sequence SEQ ID NO:277.

XX

KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.

XX

OS Homo sapiens.

XX

PN WO200012708-A2.

XX
PD 09-MAR-2000.
XX
PF 01-SEP-1999; 99WO-US020111.
XX
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099816P.
PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101476P.
PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101479P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 29-SEP-1998; 98US-0102207P.

PR	29-SEP-1998;	98US-0102240P.
PR	29-SEP-1998;	98US-0102307P.
PR	29-SEP-1998;	98US-0102330P.
PR	29-SEP-1998;	98US-0102331P.
PR	30-SEP-1998;	98US-0102484P.
PR	30-SEP-1998;	98US-0102487P.
PR	30-SEP-1998;	98US-0102570P.
PR	30-SEP-1998;	98US-0102571P.
PR	01-OCT-1998;	98US-0102684P.
PR	01-OCT-1998;	98US-0102687P.
PR	02-OCT-1998;	98US-0102965P.
PR	06-OCT-1998;	98US-0103258P.
PR	06-OCT-1998;	98US-0103449P.
PR	07-OCT-1998;	98US-0103314P.
PR	07-OCT-1998;	98US-0103315P.
PR	07-OCT-1998;	98US-0103328P.
PR	07-OCT-1998;	98US-0103395P.
PR	07-OCT-1998;	98US-0103396P.
PR	07-OCT-1998;	98US-0103401P.
PR	08-OCT-1998;	98US-0103633P.
PR	08-OCT-1998;	98US-0103678P.
PR	08-OCT-1998;	98US-0103679P.
PR	08-OCT-1998;	98US-0103711P.
PR	14-OCT-1998;	98US-0104257P.
PR	20-OCT-1998;	98US-0104987P.
PR	20-OCT-1998;	98US-0105000P.
PR	20-OCT-1998;	98US-0105002P.
PR	21-OCT-1998;	98US-0105104P.
PR	22-OCT-1998;	98US-0105169P.
PR	22-OCT-1998;	98US-0105266P.
PR	26-OCT-1998;	98US-0105693P.
PR	26-OCT-1998;	98US-0105694P.
PR	27-OCT-1998;	98US-0105807P.
PR	27-OCT-1998;	98US-0105881P.
PR	27-OCT-1998;	98US-0105882P.
PR	27-OCT-1998;	98US-0106062P.
PR	28-OCT-1998;	98US-0106023P.
PR	28-OCT-1998;	98US-0106029P.
PR	28-OCT-1998;	98US-0106030P.
PR	28-OCT-1998;	98US-0106032P.
PR	28-OCT-1998;	98US-0106033P.
PR	28-OCT-1998;	98US-0106178P.
PR	29-OCT-1998;	98US-0106248P.
PR	29-OCT-1998;	98US-0106384P.
PR	29-OCT-1998;	98US-0108500P.
PR	30-OCT-1998;	98US-0106464P.
PR	03-NOV-1998;	98US-0106856P.
PR	03-NOV-1998;	98US-0106902P.
PR	03-NOV-1998;	98US-0106905P.
PR	03-NOV-1998;	98US-0106919P.
PR	03-NOV-1998;	98US-0106932P.
PR	03-NOV-1998;	98US-0106934P.
PR	10-NOV-1998;	98US-0107783P.
PR	17-NOV-1998;	98US-0108775P.
PR	17-NOV-1998;	98US-0108779P.
PR	17-NOV-1998;	98US-0108787P.
PR	17-NOV-1998;	98US-0108788P.

Db	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDSFVAAIPST	240
Qy	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Db	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Qy	301	FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Db	301	FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Qy	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAV	420
Db	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAV	420
Qy	421	ETAQGLDGHSHLVMYLGTTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Db	421	ETAQGLDGHSHLVMYLGTTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Qy	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Db	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Qy	541	GNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Db	541	GNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Qy	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Db	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Qy	661	VKVPLTRVSGGAALAAQSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE	720
Db	661	VKVPLTRVSGGAALAAQSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE	720
Qy	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761
Db	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761

RESULT 2

AAB24084

ID AAB24084 standard; protein; 761 AA.

XX

AC AAB24084;

XX

DT 29-JAN-2001 (first entry)

XX

DE Human PRO1317 protein sequence SEQ ID NO:71.

XX

KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
 KW proliferation; tumourigenesis; identification; cancer; cytostatic;
 KW nootropic; neuroprotective; antiinflammatory; immunosuppressive;
 KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
 KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;
 KW hypothalamic disorder; glandular disorder; macrophagal disorder;
 KW epithelial disorder; stromal disorder; blastocoelic disorder;
 KW inflammatory disorder; immunologic disorder.

XX
 OS Homo sapiens.
 XX
 PN WO200053755-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 06-JAN-2000; 2000WO-US000376.
 XX
 PR 08-MAR-1999; 99WO-US005028.
 PR 02-JUN-1999; 99WO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 07-JUL-1999; 99US-0143048P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 20-DEC-1999; 99WO-US030911.
 PR 05-JAN-2000; 2000WO-US000219.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
 PI Watanabe CK, Wood WI;
 XX
 DR WPI; 2000-572270/53.
 DR N-PSDB; AAC58392.
 XX
 PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
 PT treatment, diagnosis and prevention of cancer.
 XX
 PS Claim 61; Fig 52; 286pp; English.
 XX
 CC The present invention describes an isolated antibody that binds to one of
 CC the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619,
 CC PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO1025,
 CC PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187,
 CC PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR
 CC PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The
 CC PRO polypeptides and nucleotides are useful in the treatment, diagnosis
 CC and prevention of cancer. The antibodies and other anti-tumour compounds
 CC maybe used to treat various conditions, including those characterised by
 CC overexpression and/or activation of the amplified PRO genes. Exemplary
 CC conditions or disorders to be treated with such antibodies and other
 CC compounds include benign or malignant tumours (e.g., renal, liver,
 CC kidney, bladder, breast, gastric, ovarian, colorectal, prostate,
 CC pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas,
 CC glioblastomas, and various head and neck tumours), leukaemias and
 CC lymphoid malignancies, other disorders such as neuronal, glial,
 CC astrocytal, hypothalamic and other glandular, macrophagal, epithelial,
 CC stromal and blastocoelec disorders, and inflammatory, angiogenic and
 CC immunologic disorders. AAC58242 to AAC58366 represent PCR primers and
 CC hybridisation probes used in the isolation of the human PRO sequences.
 CC AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human PRO
 CC polynucleotide and protein sequences given in the exemplification of the
 CC present invention
 XX
 SQ Sequence 761 AA;

Query Match 100.0%; Score 4031; DB 3; Length 761;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGMPRVRYAGDERRALSFFHQKG	60
Db	1	MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGMPRVRYAGDERRALSFFHQKG	60
Qy	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKSN	120
Db	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKSN	120
Qy	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP	180
Db	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP	180
Qy	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAPST	240
Db	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAPST	240
Qy	241	QVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Db	241	QVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Qy	301	FNVRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Db	301	FNVRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Qy	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMLDEQVVGTPLLVKSGVEYTRLAV	420
Db	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMLDEQVVGTPLLVKSGVEYTRLAV	420
Qy	421	ETAQGLDGHSHLVMYLGT'TTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Db	421	ETAQGLDGHSHLVMYLGT'TTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Qy	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Db	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Qy	541	GNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Db	541	GNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Qy	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Db	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Qy	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE	720
Db	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE	720
Qy	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761
Db	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761

RESULT 3

AAB66167

ID AAB66167 standard; protein; 761 AA.

XX

AC AAB66167;

XX

DT 02-APR-2001 (first entry)

XX

DE Protein of the invention #79.

XX

KW Secreted; transmembrane; gene therapy.

XX

OS Unidentified.

XX

PN WO200078961-A1.

XX

PD 28-DEC-2000.

XX

PF 18-FEB-2000; 2000WO-US004342.

XX

PR 23-JUN-1999; 99US-0141037P.

PR 20-JUL-1999; 99US-0144758P.

PR 26-JUL-1999; 99US-0145698P.

PR 01-SEP-1999; 99WO-US020111.

PR 29-OCT-1999; 99US-0162506P.

PR 30-NOV-1999; 99WO-US028313.

PR 02-DEC-1999; 99WO-US028551.

PR 16-DEC-1999; 99WO-US030095.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000376.

XX

PA (GETH) GENENTECH INC.

XX

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;

PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;

PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;

PI Williams PM, Wood WI;

XX

DR WPI; 2001-071395/08.

XX

PT Secreted and transmembrane proteins and nucleic acids designated PRO,
PT useful as hybridization probes, in chromosome and gene mapping and gene
PT therapy.

XX

PS Claim 1; Fig 158; 787pp; English.

XX

CC The present invention relates to secreted and transmembrane proteins.

CC These proteins and the DNA encoding them may be used as hybridization

CC probes, in chromosome and gene mapping and in the generation of anti-

CC sense RNA and DNA. They may also be used to generate either

CC transgenic animals or knockout animals which are in turn useful for

CC development and screening of therapeutically useful reagents. The nucleic

CC acids may also be used in gene therapy

XX

SQ Sequence 761 AA;

Query Match

100.0%; Score 4031; DB 4; Length 761;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMRVRYYAGDERRALSFFHQKG	60
Db	1	MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMRVRYYAGDERRALSFFHQKG	60
Qy	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKSN	120
Db	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKSN	120
Qy	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Db	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Qy	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST	240
Db	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST	240
Qy	241	QVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Db	241	QVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Qy	301	FNVI RHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Db	301	FNVI RHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Qy	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAV	420
Db	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAV	420
Qy	421	ETAQGLDGHSHLVMYLGT'TTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Db	421	ETAQGLDGHSHLVMYLGT'TTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Qy	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Db	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Qy	541	GNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Db	541	GNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Qy	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Db	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Qy	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVL FALVLSGALIIIVASPLRALRARGKVQGCE	720
Db	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVL FALVLSGALIIIVASPLRALRARGKVQGCE	720
Qy	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761
Db	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761

RESULT 4

AAM80295

ID AAM80295 standard; protein; 761 AA.

XX

AC AAM80295;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human protein SEQ ID NO 3947.

XX

KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukaemia;

KW nervous system disorder; arthritis; inflammation.

XX

OS Homo sapiens.

XX

PN WO200157190-A2.

XX

PD 09-AUG-2001.

XX

PF 05-FEB-2001; 2001WO-US004098.

XX

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PR 20-JUN-2000; 2000US-00598075.

PR 19-JUL-2000; 2000US-00620325.

PR 01-SEP-2000; 2000US-00654936.

PR 15-SEP-2000; 2000US-00663561.

PR 20-OCT-2000; 2000US-00693325.

PR 30-NOV-2000; 2000US-00728422.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;

PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

XX

DR WPI; 2001-476283/51.

DR N-PSDB; AAK53428.

XX

PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.

XX

PS Claim 20; Page 6209-6210; 6221pp; English.

XX

CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the

CC sequence listing were missing at the time of publication
XX
SQ Sequence 761 AA;

Query Match 100.0%; Score 4031; DB 4; Length 761;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGMPRVRYAGDERRALSFFHQKG 60
      |||
Db      1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGMPRVRYAGDERRALSFFHQKG 60

Qy     61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSN 120
      |||
Db     61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSN 120

Qy    121 ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP 180
      |||
Db    121 ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP 180

Qy    181 AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST 240
      |||
Db    181 AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST 240

Qy    241 QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP 300
      |||
Db    241 QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP 300

Qy    301 FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGTRSSAVCAFSLLDIERVFKGKYKELNKE 360
      |||
Db    301 FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGTRSSAVCAFSLLDIERVFKGKYKELNKE 360

Qy    361 TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV 420
      |||
Db    361 TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV 420

Qy    421 ETAQGLDGHSHLVMYLGTTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA 480
      |||
Db    421 ETAQGLDGHSHLVMYLGTTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA 480

Qy    481 VFVGFGGGVWRVPRANC SVYESCVDCVLARDPHCAWD PESRTCCLLSAPNLNSWKQDMER 540
      |||
Db    481 VFVGFGGGVWRVPRANC SVYESCVDCVLARDPHCAWD PESRTCCLLSAPNLNSWKQDMER 540

Qy    541 GNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE 600
      |||
Db    541 GNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE 600

Qy    601 ASSTVYNGSLLLIVQDGVGGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH 660
      |||
Db    601 ASSTVYNGSLLLIVQDGVGGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH 660

Qy    661 VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE 720
      |||
Db    661 VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE 720

Qy    721 TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA 761
```


|||||
Db 721 TLRPGEKAPLSREQHLQSPKECRTSASDVADANNCLGTEVA 761

RESULT 5

AAB66043

ID AAB66043 standard; protein; 761 AA.

XX

AC AAB66043;

XX

DT 30-MAR-2001 (first entry)

XX

DE Human TANGO 265.

XX

KW TANGO protein; INTERCEPT protein; neurological disorder;

KW central nervous system; focal brain disorder; bipolar affective disorder;

KW global-diffuse cerebral disorder; cerebrovascular; Alzheimer's disease;

KW senile dementia; Huntington's disease; amyotrophic lateral sclerosis;

KW Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep;

KW neuropsychiatric; psychoactive substance use; anxiety.

XX

OS Homo sapiens.

XX

PN WO200077239-A2.

XX

PD 21-DEC-2000.

XX

PF 24-MAY-2000; 2000WO-US014858.

XX

PR 14-JUN-1999; 99US-00333159.

XX

PA (MILL-) MILLENNIUM PHARM INC.

XX

PI McCarthy SA, Fraser CC, Sharp JD, Barnes TM;

XX

DR WPI; 2001-032313/04.

DR N-PSDB; AAF45125, AAF45126.

XX

PT TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for

PT screening assays and diagnostic assays and for the treatment of

PT neurological diseases such as Alzheimer's, Parkinson's and Huntington's

PT disease.

XX

PS Claim 8; Fig 3; 359pp; English.

XX

CC The present invention relates to TANGO or INTERCEPT proteins and coding

CC sequences (see AAF45121-F45136 and AAF45138-F45139 and AAB66031-B66057,

CC AAB66064-B66083 and AAB66085). The TANGO/INTERCEPT proteins and coding

CC sequences are useful for the treatment of neurological disorders such as

CC central nervous system (CNS) disorders, CNS-related disorders, focal

CC brain disorders, global-diffuse cerebral disorders and other neurological

CC and cerebrovascular disorders. The CNS disorders include Alzheimer's

CC disease, senile dementia, Huntington's disease, amyotrophic lateral

CC sclerosis, Parkinson's, Gilles de la Tourette's syndrome, autonomic

CC function disorders such as hypertension and sleep disorders,

CC neuropsychiatric disorders, psychoactive substance use disorders,

CC anxiety, and bipolar affective disorder

SQ Sequence 761 AA;

Qy	1	MALPALGLDPWSLLGLFLFQLLQLLLPPTTTAGGGGQGMPRVRYAGDERRALSFFHQKG	60
Db	1	MALPALGLDPWSLLGLFLFQLLQLLLPPTTTAGGGGQGMPRVRYAGDERRALSFFHQKG	60
Qy	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKS	120
Db	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKS	120
Qy	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Db	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Qy	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAPST	240
Db	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAPST	240
Qy	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Db	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Qy	301	FNVIRHAVLLPADSPTAPIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Db	301	FNVIRHAVLLPADSPTAPIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Qy	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAV	420
Db	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAV	420
Qy	421	ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Db	421	ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Qy	481	VFVGFGSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Db	481	VFVGFGSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Qy	541	GNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Db	541	GNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Qy	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Db	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Qy	661	VKVPLTRVSGGAALAAQOSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE	720
Db	661	VKVPLTRVSGGAALAAQOSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE	720
Qy	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761

Db

721 TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA 761

RESULT 6

ABG72615

ID ABG72615 standard; protein; 761 AA.

XX

AC ABG72615;

XX

DT 12-FEB-2003 (first entry)

XX

DE Human cytokine or cell proliferation/differentiation protein #5.

XX

KW Human; cytokine; cell proliferation; cell differentiation; anaemia;

KW wound; ulcer; thrombocytopaenia; osteoporosis; osteoarthritis;

KW inflammation; Alzheimer's disease; Parkinson's disease; stroke;

KW Huntington's disease; amyotrophic lateral sclerosis; HIV;

KW immune deficiency; human immunodeficiency virus infection;

KW severe combined immunodeficiency; infection; autoimmune disorder;

KW rheumatoid arthritis; Guillain-Barre syndrome; graft-versus-host disease;

KW cancer; thyroid cancer; lung cancer; small cell carcinoma;

KW Kaposi's sarcoma; brain tumour; prostate cancer; ovarian cancer;

KW leukaemia; inflammatory disorder; inflammatory bowel disease;

KW Crohn's disease; food supplement.

XX

OS Homo sapiens.

XX

PN US2002137044-A1.

XX

PD 26-SEP-2002.

XX

PF 30-JAN-2001; 2001US-00774434.

XX

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

XX

PA (TANG/) TANG Y T.

PA (ZHOU/) ZHOU P.

PA (GOOD/) GOODRICH R.

PA (LIUC/) LIU C.

PA (ASUN/) ASUNDI V.

PA (WEHR/) WEHRMAN T.

PA (YANG/) YANG Y.

PA (DRMA/) DRMANAC R T.

XX

PI Tang YT, Zhou P, Goodrich R, Liu C, Asundi V, Wehrman T, Yang Y;

PI Drmanac RT;

XX

DR WPI; 2003-110596/10.

DR N-PSDB; ABX13628.

XX

PT New polynucleotides for diagnosing, treating or preventing e.g. anemia,

PT wounds, ulcers, thrombocytopenia, osteoporosis, inflammations,

PT Alzheimer's disease, stroke, autoimmune disorders or cancers.

XX

PS Claim 19; Page 57-59; 63pp; English.

XX

CC The invention relates to an isolated polynucleotide encoding a cytokine
 CC or cell proliferation/differentiation-related protein (or the mature
 CC protein or active domain), sequences greater than 90% identical to it or
 CC sequences complementary to it. Also included are the encoded proteins,
 CC expression vectors, transformed host cells, antibodies, and identifying a
 CC compound that binds to the polypeptide. The polynucleotide, polypeptides
 CC encoded by it, or antibodies to the polypeptides are useful in
 CC therapeutic, diagnostic or research methods. They are particularly useful
 CC for diagnosing, treating or preventing e.g. anaemias, wounds, ulcers,
 CC thrombocytopaenia, osteoporosis, osteoarthritis, inflammations,
 CC Alzheimer's disease, Parkinson's disease, Huntington's disease,
 CC amyotrophic lateral sclerosis, stroke, immune deficiencies (e.g. human
 CC immunodeficiency virus (HIV), severe combined immunodeficiency or
 CC infections), autoimmune disorders (e.g. rheumatoid arthritis, Guillain-
 CC Barre syndrome or graft-versus-host disease), cancers (e.g. thyroid
 CC cancer, lung cancers, small cell carcinoma, Kaposi's sarcoma, brain
 CC tumours, prostate cancer, ovarian cancer or leukaemias), or inflammatory
 CC disorders (e.g. inflammatory bowel disease or Crohn's disease). The
 CC polynucleotides and proteins are useful for screening peptides or small
 CC molecule inhibitors or agonists that are useful for treating these
 CC diseases. The polypeptide is also useful as molecular markers, or as a
 CC food supplement. The present sequence is a cytokine or cell
 CC proliferation/differentiation-related protein of the invention
 XX
 SQ Sequence 761 AA;

Query Match 100.0%; Score 4031; DB 6; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGMPRVRYAGDERRALSFFHQKG	60
Db	1	MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGMPRVRYAGDERRALSFFHQKG	60
Qy	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKSN	120
Db	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKSN	120
Qy	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Db	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Qy	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST	240
Db	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST	240
Qy	241	QVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Db	241	QVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Qy	301	FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Db	301	FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Qy	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV	420
Db	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV	420

Qy	421	ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Db	421	ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Qy	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPE SRTCCLLSAPNLNSWKQDMER	540
Db	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPE SRTCCLLSAPNLNSWKQDMER	540
Qy	541	GNPEWACASGPM SRS LRPQSRPQIIKEVLAVPNSILELPCPHLSALASYW SHGPAAVPE	600
Db	541	GNPEWACASGPM SRS LRPQSRPQIIKEVLAVPNSILELPCPHLSALASYW SHGPAAVPE	600
Qy	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Db	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Qy	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE	720
Db	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE	720
Qy	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761
Db	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761

RESULT 7

ABU08366

ID ABU08366 standard; protein; 761 AA.

XX

AC ABU08366;

XX

DT 03-JUN-2003 (first entry)

XX

DE Amino acid sequence for human TANGO 265.

XX

KW Human; TANGO 265; INTERCEPT; cellular process; tissue typing;
 KW forensic biology; cellular protease activity; cell interaction;
 KW development; blood disorder; haematopoietic cell-related disorder;
 KW growth; cell proliferation; cell differentiation; gamma delta T-cell;
 KW immune system; metabolic disorder; homeostatic disorder; anaemia;
 KW developmental bone disorder; osteoporosis; bacterial infection;
 KW thrombocytopaenia; renal failure; liver disease; cystic fibrosis;
 KW obesity; cancer; bronchitis; asthma; emphysema; pulmonary oedema;
 KW respiratory distress syndrome; osteopathic; antibacterial; antianaemic;
 KW thrombolytic; nephrotropic; antiobesity; hepatotropic; cytostatic;
 KW antiinflammatory; antiasthmatic.

XX

OS Homo sapiens.

XX

PN US2002182675-A1.

XX

PD 05-DEC-2002.

XX

PF 25-OCT-2001; 2001US-00042431.

XX

PR 14-JUN-1999; 99US-00333159.

Qy	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Db	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Qy	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST	240
Db	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST	240
Qy	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Db	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Qy	301	FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Db	301	FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Qy	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMLDEQVVGTPLLVKSGVEYTRLAV	420
Db	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMLDEQVVGTPLLVKSGVEYTRLAV	420
Qy	421	ETAQGLDGHSHLVMYLGTTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Db	421	ETAQGLDGHSHLVMYLGTTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Qy	481	VFVGFGGCVWRVPRANC SVYESCVDCVLARDPHCAWDPE SRTCCLLSAPNLNSWKQDMER	540
Db	481	VFVGFGGCVWRVPRANC SVYESCVDCVLARDPHCAWDPE SRTCCLLSAPNLNSWKQDMER	540
Qy	541	GNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Db	541	GNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Qy	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Db	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Qy	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVL FALVLSGALIILVASPLRALRARGKVQGCE	720
Db	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVL FALVLSGALIILVASPLRALRARGKVQGCE	720
Qy	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761
Db	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761

RESULT 8

ABO32703

ID ABO32703 standard; protein; 761 AA.

XX

AC ABO32703;

XX

DT 17-SEP-2003 (first entry)

XX

DE Secreted polypeptide-related protein #84.

XX

KW Human; TANGO; INTERCEPT; secreted polypeptide; immune disorder;

KW hormonal disorder; proliferative disorder; cancer; thyroid disorder;

KW diabetes; multiple sclerosis; lupus; neurological disorder; anaemia;
 KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
 KW myocardial infarction; congestive heart disease; blood platelet disorder;
 KW thrombocytopenia; blood vessel; atherosclerosis; vasculitis.
 XX
 OS Homo sapiens.
 XX
 PN US2003022279-A1.
 XX
 PD 30-JAN-2003.
 XX
 PF 12-JAN-2001; 2001US-00759130.
 XX
 PR 14-JUN-1999; 99US-00333159.
 PR 29-JUN-1999; 99US-00342364.
 PR 10-SEP-1999; 99US-00393996.
 PR 19-OCT-1999; 99US-00420707.
 PR 07-JAN-2000; 2000US-00479249.
 PR 27-APR-2000; 2000US-00559497.
 PR 24-MAY-2000; 2000US-00578063.
 PR 16-JUN-2000; 2000US-00596194.
 PR 23-JUN-2000; 2000US-00602871.
 PR 30-JUN-2000; 2000US-00608452.
 XX
 PA (FRAS/) FRASER C C.
 PA (BARN/) BARNES T M.
 PA (SHAR/) SHARP J D.
 PA (KIRS/) KIRST S J.
 PA (MYER/) MYERS P S.
 PA (LEIB/) LEIBY K R.
 PA (HOLT/) HOLTZMAN D A.
 PA (MCCA/) MCCARTHY S A.
 PA (WRIG/) WRIGHTON N.
 PA (MACK/) MACKAY C R.
 PA (GOOD/) GOODEARL A D J.
 XX
 PI Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;
 PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;
 XX
 DR WPI; 2003-456290/43.
 DR N-PSDB; ACD66780, ACD66781.
 XX
 PT New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202,
 PT TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or
 PT treating disorders such as cancer, diabetes or atherosclerosis, and in
 PT forensic biology.
 XX
 PS Claim 9; Fig 27A-27E; 482pp; English.
 XX
 CC The invention relates to secreted polypeptide-related proteins and
 CC nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The
 CC nucleic acids, proteins and antibodies specific to the proteins are
 CC useful in screening assays, predictive medicine (e.g. diagnostic assays,
 CC prognostic assays, monitoring clinical trials and pharmacogenetics) and
 CC prophylactic and therapeutic methods. The sequences are used in
 CC diagnosing, preventing or treating proliferative disorders (e.g.
 CC cancers), hormonal disorders (e.g. diabetes or thyroid disorders), immune

CC disorders (e.g. multiple sclerosis or lupus), neurological disorders
CC (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular
CC disorders (e.g. myocardial infarction or congestive heart disease), blood
CC platelet disorders (e.g. thrombocytopenia or anaemia) and disorders
CC involving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic
CC acids may also be used in chromosome mapping, tissue typing and forensic
CC biology, and as surrogate markers. This sequence represents a secreted
CC polypeptide-related protein of the invention. Note: The sequence data for
CC this patent was obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html

XX

SQ Sequence 761 AA;

Query Match 100.0%; Score 4031; DB 6; Length 761;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGMPRVRYAGDERRALSFFHQKG	60
Db	1	MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGMPRVRYAGDERRALSFFHQKG	60
Qy	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSN	120
Db	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSN	120
Qy	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP	180
Db	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP	180
Qy	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDSFVAaipst	240
Db	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDSFVAaipst	240
Qy	241	QVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Db	241	QVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Qy	301	FNvirHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Db	301	FNvirHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Qy	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV	420
Db	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV	420
Qy	421	ETAQGLDGSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Db	421	ETAQGLDGSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Qy	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPEsrtCCLLSAPNlnSWKQDMER	540
Db	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPEsrtCCLLSAPNlnSWKQDMER	540
Qy	541	GNPEWACASGPMsRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYYWSHGPAAVPE	600
Db	541	GNPEWACASGPMsRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYYWSHGPAAVPE	600

Qy 601 ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH 660
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 Qy 661 VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFAVLVSGALIILVASPLRALRARGKVQGCE 720
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 Qy 721 TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA 761
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 Db 721 TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA 761

RESULT 9

ABO33660

ID ABO33660 standard; protein; 761 AA.

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AC ABO33660;

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DT 17-SEP-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO1317.

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KW Human; secreted and transmembrane protein; PRO; angiogenesis;
 KW endothelial cell proliferation; wound healing; immune response;
 KW T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;
 KW cardiac insufficiency disorder; calcium flux; inflammation;
 KW vascular endothelial growth factor-stimulated proliferation;
 KW mammalian kidney mesangial cell proliferation; Berger disease;
 KW nephropathy; Schanlein-Henoch purpura; celiac disease; Crohn's disease;
 KW dermatitis herpetiformis; diabetes; haemoglobin switch; insulinaemia;
 KW pancreatic beta-cell precursor cell differentiation; thalassemias;
 KW obesity; auditory hair cell regeneration; hearing loss; bone disorder;
 KW cartilage disorder; sports injury; arthritis.

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OS Homo sapiens.

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PN US2003073130-A1.

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PD 17-APR-2003.

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PF 11-DEC-2001; 2001US-00015869.

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PR 01-SEP-1998; 98US-0098716P.
 PR 01-SEP-1998; 98US-0098723P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 01-SEP-1998; 98US-0098750P.
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 PR 02-SEP-1998; 98US-0098821P.
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 PR 09-SEP-1998; 98US-0099536P.
 PR 09-SEP-1998; 98US-0099596P.
 PR 09-SEP-1998; 98US-0099598P.
 PR 09-SEP-1998; 98US-0099602P.
 PR 09-SEP-1998; 98US-0099642P.
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 PR 10-SEP-1998; 98US-0099754P.

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PR	10-SEP-1998;	98US-0099816P.
PR	15-SEP-1998;	98US-0100385P.
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PR	17-NOV-1998;	98US-0108779P.
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PR	22-DEC-1998;	98US-0113296P.
PR	30-DEC-1998;	98US-0114223P.
PR	05-JAN-1999;	99WO-US000106.
PR	16-APR-1999;	99US-0129674P.
PR	23-JUN-1999;	99US-0141037P.
PR	20-JUL-1999;	99US-0144758P.

PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021194.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.

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PA (GETH) GENENTECH INC.

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PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;

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DR WPI; 2003-585293/55.

DR N-PSDB; ACD68436.

XX

PT Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,
 PT PRO1787 that modulate glucose or free fatty acid uptake by skeletal
 PT muscle cells, and are useful for treating diabetes, hyper- or hypo-

Query Match 100.0%; Score 4031; DB 6; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60
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 Db 1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60
 Qy 61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKS 120
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 Db 61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKS 120

Qy	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Db	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Qy	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST	240
Db	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST	240
Qy	241	QVYVFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Db	241	QVYVFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Qy	301	FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Db	301	FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Qy	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLLVKSGVEYTRLAV	420
Db	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLLVKSGVEYTRLAV	420
Qy	421	ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Db	421	ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Qy	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Db	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Qy	541	GNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Db	541	GNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Qy	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Db	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Qy	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIIILVASPLRALRARGKVQGCE	720
Db	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIIILVASPLRALRARGKVQGCE	720
Qy	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761
Db	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761

RESULT 10

ABO44513

ID ABO44513 standard; protein; 761 AA.

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AC ABO44513;

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DT 01-OCT-2003 (first entry)

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DE Human secreted/transmembrane protein PRO1317.

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KW Human; secreted protein; transmembrane protein; PRO; vulnerary; cardiant;
 KW antidiabetic; anorectic; antiarthritic; angiogenesis; cancer;

KW adrenal cortical capillary; endothelial cell growth; wound healing;
KW stimulated T-lymphocyte proliferation; immune response suppression;
KW neonatal heart hypertrophy; cardiac insufficiency disorder;
KW vascular endothelial growth factor; inflammation; mononuclear cell;
KW eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;
KW chondrocyte redifferentiation; bone disorder; cartilage disorder;
KW sports injury; arthritis.

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OS Homo sapiens.

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PN US2003044841-A1.

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PD 06-MAR-2003.

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PF 06-DEC-2001; 2001US-00006856.

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PR 01-SEP-1998; 98US-0098716P.

PR 01-SEP-1998; 98US-0098723P.

PR 01-SEP-1998; 98US-0098749P.

PR 01-SEP-1998; 98US-0098750P.

PR 02-SEP-1998; 98US-0098803P.

PR 02-SEP-1998; 98US-0098821P.

PR 02-SEP-1998; 98US-0098843P.

PR 09-SEP-1998; 98US-0099536P.

PR 09-SEP-1998; 98US-0099596P.

PR 09-SEP-1998; 98US-0099598P.

PR 09-SEP-1998; 98US-0099602P.

PR 09-SEP-1998; 98US-0099642P.

PR 10-SEP-1998; 98US-0099741P.

PR 10-SEP-1998; 98US-0099754P.

PR 10-SEP-1998; 98US-0099763P.

PR 10-SEP-1998; 98US-0099792P.

PR 10-SEP-1998; 98US-0099808P.

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PR	07-OCT-1998;	98US-0103401P.
PR	08-OCT-1998;	98US-0103633P.
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PR	14-OCT-1998;	98US-0104257P.
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PR	22-OCT-1998;	98US-0105266P.
PR	26-OCT-1998;	98US-0105693P.
PR	26-OCT-1998;	98US-0105694P.
PR	27-OCT-1998;	98US-0105807P.
PR	27-OCT-1998;	98US-0105881P.
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PR 20-JUL-1999; 99US-0144758P.
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PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
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PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.

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Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPWPASDRKKSECAFKKSN	120
Db	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPWPASDRKKSECAFKKSN	120
Qy	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP	180
Db	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP	180
Qy	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAaipst	240
Db	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAaipst	240
Qy	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Db	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Qy	301	FNvirHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
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Qy	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV	420
Db	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV	420
Qy	421	ETAQGLDGHSHLVMYLGTTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Db	421	ETAQGLDGHSHLVMYLGTTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Qy	481	VFVGFGSGGVWRVPRANCsvYESCVDCVLARDPHCAWDPEsRtCCLLSAPnLNSwKQdMER	540

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Db      661 VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFLVLSGALIIILVASPLRALRARGKVQGCE 720
Qy      721 TLRPGEKAPLSREQHLQSPKECRTSASDVEDADNNCLGTEVA 761
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Db      721 TLRPGEKAPLSREQHLQSPKECRTSASDVEDADNNCLGTEVA 761

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RESULT 11

ABO33537

ID ABO33537 standard; protein; 761 AA.

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AC ABO33537;

XX

DT 17-SEP-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PRO1317.

XX

KW Human; secreted and transmembrane protein; PRO; gene therapy; vaccine;

KW tissue typing; chromosome identification; vaccine.

XX

OS Homo sapiens.

XX

PN US2003073129-A1.

XX

PD 17-APR-2003.

XX

PF 04-SEP-2001; 2001US-00946374.

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PR 01-SEP-1998; 98US-0098716P.

PR 01-SEP-1998; 98US-0098723P.

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 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
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 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
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 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.

XX

PA (GETH) GENENTECH INC.

XX

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;

XX

DR WPI; 2003-585292/55.

DR N-PSDB; ACD68082.

XX

PT Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
 PT preparation of a medicament for treating a condition responsive to PRO
 PT polypeptide, and as therapeutic agents e.g. vaccines.

XX

PS Claim 12; Fig 158; 561pp; English.

XX

CC The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I), having at least 80% sequence identity to a sequence

Query Match 100.0%; Score 4031; DB 7; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60

Db	1	MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG	60
Qy	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSN	120
Db	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSN	120
Qy	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP	180
Db	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP	180
Qy	181	AHKHTAVLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST	240
Db	181	AHKHTAVLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST	240
Qy	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Db	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Qy	301	FNVI RHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Db	301	FNVI RHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Qy	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV	420
Db	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV	420
Qy	421	ETAQGLDGHSHLVMYLGTTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Db	421	ETAQGLDGHSHLVMYLGTTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Qy	481	VFVGFSGGVWRVPRANCSVYESCVCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Db	481	VFVGFSGGVWRVPRANCSVYESCVCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Qy	541	GNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Db	541	GNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Qy	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Db	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Qy	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE	720
Db	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE	720
Qy	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761
Db	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761

RESULT 12

ADC18146

ID ADC18146 standard; protein; 761 AA.

XX

AC ADC18146;

XX
DT 18-DEC-2003 (first entry)
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DE Human PRO polypeptide #79.
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KW Human; PRO; protein electrophoresis; chromosome mapping; gene mapping;
KW genetic disorder.
XX
OS Homo sapiens.
XX
PN US2003064925-A1.
XX
PD 03-APR-2003.
XX
PF 10-DEC-2001; 2001US-00013907.
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PR 01-SEP-1998; 98US-0098716P.
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PR	07-OCT-1998;	98US-0103314P.
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PR	14-OCT-1998;	98US-0104257P.
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PR	20-OCT-1998;	98US-0105000P.
PR	20-OCT-1998;	98US-0105002P.
PR	21-OCT-1998;	98US-0105104P.
PR	22-OCT-1998;	98US-0105169P.
PR	22-OCT-1998;	98US-0105266P.
PR	26-OCT-1998;	98US-0105693P.
PR	26-OCT-1998;	98US-0105694P.
PR	27-OCT-1998;	98US-0105807P.
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PR	27-OCT-1998;	98US-0105882P.
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PR	28-OCT-1998;	98US-0106023P.
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PR	28-OCT-1998;	98US-0106030P.
PR	28-OCT-1998;	98US-0106032P.
PR	28-OCT-1998;	98US-0106033P.
PR	28-OCT-1998;	98US-0106178P.
PR	29-OCT-1998;	98US-0106248P.
PR	29-OCT-1998;	98US-0106384P.
PR	29-OCT-1998;	98US-0108500P.

PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
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PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.

PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;
 XX
 DR WPI; 2003-555602/52.
 DR N-PSDB; ADC18145.
 XX
 PT Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
 PT preparation of a medicament for treating a condition responsive to PRO
 PT polypeptide, and as therapeutic agents e.g. vaccines.
 XX
 PS Claim 12; SEQ ID NO 277; 555pp; English.
 XX
 CC The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The sequences are useful in the preparation of a
 CC medicament for treating a condition responsive to a PRO polypeptide. The
 CC polypeptides are useful in a number of functional biological assays, as
 CC molecular weight markers for protein electrophoresis and as therapeutic

Query Match 100.0%; Score 4031; DB 7; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MALPALGLDPWSLLGLFLFQLLQLLP	TTAGGGGQGPM	PRVRYAGDERRALSFFHQKG	60
Db	1	MALPALGLDPWSLLGLFLFQLLQLLP	TTAGGGGQGPM	PRVRYAGDERRALSFFHQKG	60
Qy	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSN			120
Db	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSN			120
Qy	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP			180
Db	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP			180
Qy	181	AHKHTAVLVDGMLYSGTMNIFLGSEPIILMRTLGSQPVLKTDNFLRWLHHDASFVAaipst			240
Db	181	AHKHTAVLVDGMLYSGTMNIFLGSEPIILMRTLGSQPVLKTDNFLRWLHHDASFVAaipst			240
Qy	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQILLCTQPGQLP			300
Db	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQILLCTQPGQLP			300
Qy	301	FNvirHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE			360
Db	301	FNvirHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE			360
Qy	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTfMKDHFLMDEQVVGTPLLVKSGVEYTRLAV			420

Db 361 TSRWTTYRGPETNPRPGSCSVGFPSSDKALTFMKDHFLMDEQVVGTPLLLVKSGVEYTRLAV 420
 Qy 421 ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA 480
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 Qy 481 VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER 540
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 Db 481 VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER 540
 Qy 541 GNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPE 600
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 Db 541 GNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPE 600
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 Qy 661 VKVPLTRVSGGAALAAQQSYWPHFVTVTVL FALVLSGALIILVASPLRALRARGKVQGCE 720
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 Qy 721 TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA 761
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 Db 721 TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA 761

RESULT 13

ADD70792

ID ADD70792 standard; protein; 761 AA.

XX

AC ADD70792;

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DT 15-JAN-2004 (first entry)

XX

DE Human secreted/transmembrane protein PRO1317.

XX

KW Human; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;

KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.

XX

OS Homo sapiens.

XX

PN US2003099625-A1.

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PD 29-MAY-2003.

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PF 12-DEC-2001; 2001US-00015386.

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PR 01-SEP-1998; 98US-0098716P.

PR 01-SEP-1998; 98US-0098723P.

PR 01-SEP-1998; 98US-0098749P.

PR 01-SEP-1998; 98US-0098750P.

PR 02-SEP-1998; 98US-0098803P.

PR	02-SEP-1998;	98US-0098821P.
PR	02-SEP-1998;	98US-0098843P.
PR	09-SEP-1998;	98US-0099536P.
PR	09-SEP-1998;	98US-0099596P.
PR	09-SEP-1998;	98US-0099598P.
PR	09-SEP-1998;	98US-0099602P.
PR	09-SEP-1998;	98US-0099642P.
PR	10-SEP-1998;	98US-0099741P.
PR	10-SEP-1998;	98US-0099754P.
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PR	10-SEP-1998;	98US-0099792P.
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PR	15-SEP-1998;	98US-0100390P.
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PR	18-SEP-1998;	98US-0101014P.
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PR	23-SEP-1998;	98US-0101471P.
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PR	06-OCT-1998;	98US-0103449P.
PR	07-OCT-1998;	98US-0103314P.
PR	07-OCT-1998;	98US-0103315P.
PR	07-OCT-1998;	98US-0103328P.
PR	07-OCT-1998;	98US-0103395P.
PR	07-OCT-1998;	98US-0103396P.
PR	07-OCT-1998;	98US-0103401P.
PR	08-OCT-1998;	98US-0103633P.
PR	08-OCT-1998;	98US-0103678P.
PR	08-OCT-1998;	98US-0103679P.
PR	08-OCT-1998;	98US-0103711P.
PR	14-OCT-1998;	98US-0104257P.
PR	20-OCT-1998;	98US-0104987P.
PR	20-OCT-1998;	98US-0105000P.
PR	20-OCT-1998;	98US-0105002P.
PR	21-OCT-1998;	98US-0105104P.
PR	22-OCT-1998;	98US-0105169P.
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PR	30-OCT-1998;	98US-0106464P.
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PR	17-NOV-1998;	98US-0108802P.
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PR	17-NOV-1998;	98US-0108925P.
PR	18-NOV-1998;	98US-0108848P.
PR	18-NOV-1998;	98US-0108849P.
PR	18-NOV-1998;	98US-0108850P.

PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.

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PA (GETH) GENENTECH INC.

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PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;

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DR WPI; 2003-874602/81.

DR N-PSDB; ADD70791.

XX

PT Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555,
PT PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle
PT cells and are useful for treating diabetes or hyper- or hypo-insulinemia.

XX

PS Claim 12; SEQ ID NO 277; 553pp; English.

XX

CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 4031; DB 7; Length 761;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG	60
Db	1	MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG	60
Qy	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSN	120
Db	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSN	120
Qy	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Db	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Qy	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDAFVAAPST	240
Db	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDAFVAAPST	240
Qy	241	QVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Db	241	QVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Qy	301	FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Db	301	FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Qy	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAV	420
Db	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAV	420
Qy	421	ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Db	421	ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Qy	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Db	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Qy	541	GNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Db	541	GNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Qy	601	ASSTVYNGSLLLIVQDGVGGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Db	601	ASSTVYNGSLLLIVQDGVGGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Qy	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE	720
Db	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE	720
Qy	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761
Db	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761

RESULT 14

ADD39869

ID ADD39869 standard; protein; 761 AA.

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AC ADD39869;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human secreted/transmembrane protein PRO1317.

XX

KW Human; secreted protein; transmembrane protein; PRO; tumour;

KW immune response; cardiac insufficiency disorder; calcium flux;

KW umbilical vein endothelial cell; bone disorder; cartilage disorder;

KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;

KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.

XX

OS Homo sapiens.

XX

PN US2003083462-A1.

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PD 01-MAY-2003.

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PF 10-DEC-2001; 2001US-00013913.

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PR 05-JAN-1999; 99WO-US000106.

PR 01-SEP-1999; 99WO-US020111.

PR 15-SEP-1999; 99WO-US021194.

PR 30-NOV-1999; 99WO-US028313.

PR 02-DEC-1999; 99WO-US028551.

PR 16-DEC-1999; 99WO-US030095.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004342.

PR 24-FEB-2000; 2000WO-US005004.

PR 02-MAR-2000; 2000WO-US005841.

PR 15-MAR-2000; 2000WO-US006884.

PR 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WO-US014042.

PR 30-MAY-2000; 2000WO-US014941.

PR 02-JUN-2000; 2000WO-US015264.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 08-NOV-2000; 2000WO-US030952.

PR 10-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032678.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-MAR-2001; 2001WO-US006666.

PR 01-JUN-2001; 2001WO-US017800.

PR 20-JUN-2001; 2001WO-US019692.

PR 29-JUN-2001; 2001WO-US021066.

PR 09-JUL-2001; 2001WO-US021735.

PR 04-SEP-2001; 2001US-00946374.

XX

PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;
 XX
 DR WPI; 2003-755122/71.
 DR N-PSDB; ADD39868.
 XX
 PT New secreted and transmembrane PRO polypeptides useful for treating
 PT cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyper- or
 PT hypo-insulinemia, sports injuries and arthritis.
 XX
 PS Claim 12; SEQ ID NO 277; 557pp; English.
 XX
 CC The invention relates to an isolated PRO polypeptide (secreted or
 CC transmembrane protein) having at least 80% amino acid sequence identity
 CC to an amino acid sequence chosen from 123 fully defined sequences as
 CC given in the specification (including their extracellular domains either
 CC or without their associated signal peptides. Also include are the
 CC nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a
 CC host cell comprising the vector, producing PRO, a chimaeric molecule
 CC comprising PRO fused to a heterologous amino acid sequence, and an anti-
 CC PRO antibody. Pro is useful as molecular weight markers for protein
 CC electrophoresis and also for chromosome identification. PRO is also
 CC useful for tissue typing. PRO and PRO NA are useful as hybridisation
 CC probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is
 CC useful for generating transgenic animals or knock-out animals which are
 CC useful in development and screening useful reagents. PRO NA is also
 CC useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are
 CC useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410
 CC polypeptides are useful for suppressing immune response. PRO1246
 CC polypeptide is useful for treating cardiac insufficiency disorders.
 CC PRO1246 polypeptide is also useful for treating tumours. PRO1246 and
 CC PRO1561 polypeptide are useful for stimulating calcium flux in human
 CC umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474
 CC polypeptides are useful for treating bone and/or cartilage disorders
 CC (e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1418
 CC polypeptides are useful for treating diabetes in skeletal muscle cells
 CC and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for
 CC treating Berger disease or other nephropathies associated with Schonlein-
 CC Henoch purpura, coeliac disease, dermatitis, herpetiformis or Crohn's
 CC disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418,
 CC PRO1410 and PRO1575 are useful in treating thalassaemias. The present
 CC sequence represents a PRO protein of the invention.
 XX
 SQ Sequence 761 AA;

Query Match 100.0%; Score 4031; DB 7; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGMPRVRYAGDERRALSFFHQKG 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGMPRVRYAGDERRALSFFHQKG 60

Qy	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSN	120
Db	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSN	120
Qy	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Db	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Qy	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAaipst	240
Db	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAaipst	240
Qy	241	QVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Db	241	QVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Qy	301	FNvirHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Db	301	FNvirHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Qy	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV	420
Db	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV	420
Qy	421	ETAQGLDGHSHLVMYLGTTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Db	421	ETAQGLDGHSHLVMYLGTTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Qy	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPEsRTCCLLSAPNLNSWKQDMER	540
Db	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPEsRTCCLLSAPNLNSWKQDMER	540
Qy	541	GNPEWACASGPMsRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYYWSHGPAAVPE	600
Db	541	GNPEWACASGPMsRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYYWSHGPAAVPE	600
Qy	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Db	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Qy	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVLfALVLsgALIILVASPLRALRARGKVQGCE	720
Db	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVLfALVLsgALIILVASPLRALRARGKVQGCE	720
Qy	721	TLRPGEKAPLSREQHLQSPKECRTsASDVDADNNCLGTEVA	761
Db	721	TLRPGEKAPLSREQHLQSPKECRTsASDVDADNNCLGTEVA	761

RESULT 15

ADD70315

ID ADD70315 standard; protein; 761 AA.

XX

AC ADD70315;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human secreted/transmembrane protein PRO1317.
 XX
 KW Human; secreted protein; transmembrane protein; PRO; tumour;
 KW immune response; cardiac insufficiency disorder; calcium flux;
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
 KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
 KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.
 XX
 OS Homo sapiens.
 XX
 PN US2003054406-A1.
 XX
 PD 20-MAR-2003.
 XX
 PF 06-DEC-2001; 2001US-00006818.
 XX
 PR 01-SEP-1998; 98US-0098716P.
 PR 01-SEP-1998; 98US-0098723P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 01-SEP-1998; 98US-0098750P.
 PR 02-SEP-1998; 98US-0098803P.
 PR 02-SEP-1998; 98US-0098821P.
 PR 02-SEP-1998; 98US-0098843P.
 PR 09-SEP-1998; 98US-0099536P.
 PR 09-SEP-1998; 98US-0099596P.
 PR 09-SEP-1998; 98US-0099598P.
 PR 09-SEP-1998; 98US-0099602P.
 PR 09-SEP-1998; 98US-0099642P.
 PR 10-SEP-1998; 98US-0099741P.
 PR 10-SEP-1998; 98US-0099754P.
 PR 10-SEP-1998; 98US-0099763P.
 PR 10-SEP-1998; 98US-0099792P.
 PR 10-SEP-1998; 98US-0099808P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98US-0099815P.
 PR 10-SEP-1998; 98US-0099816P.
 PR 15-SEP-1998; 98US-0100385P.
 PR 15-SEP-1998; 98US-0100388P.
 PR 15-SEP-1998; 98US-0100390P.
 PR 16-SEP-1998; 98US-0100584P.
 PR 16-SEP-1998; 98US-0100627P.
 PR 16-SEP-1998; 98US-0100661P.
 PR 16-SEP-1998; 98US-0100662P.
 PR 16-SEP-1998; 98US-0100664P.
 PR 17-SEP-1998; 98US-0100683P.
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 PR 17-SEP-1998; 98US-0100710P.
 PR 17-SEP-1998; 98US-0100711P.
 PR 17-SEP-1998; 98US-0100919P.
 PR 17-SEP-1998; 98US-0100930P.
 PR 18-SEP-1998; 98US-0100848P.
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 PR 18-SEP-1998; 98US-0101014P.
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 PR 18-SEP-1998; 98US-0101071P.
 PR 22-SEP-1998; 98US-0101279P.

PR	23-SEP-1998;	98US-0101471P.
PR	23-SEP-1998;	98US-0101472P.
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PR	24-SEP-1998;	98US-0101738P.
PR	24-SEP-1998;	98US-0101741P.
PR	24-SEP-1998;	98US-0101743P.
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PR	24-SEP-1998;	98US-0101916P.
PR	29-SEP-1998;	98US-0102207P.
PR	29-SEP-1998;	98US-0102240P.
PR	29-SEP-1998;	98US-0102307P.
PR	29-SEP-1998;	98US-0102330P.
PR	29-SEP-1998;	98US-0102331P.
PR	30-SEP-1998;	98US-0102484P.
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PR	30-SEP-1998;	98US-0102570P.
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PR	01-OCT-1998;	98US-0102684P.
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PR	06-OCT-1998;	98US-0103449P.
PR	07-OCT-1998;	98US-0103314P.
PR	07-OCT-1998;	98US-0103315P.
PR	07-OCT-1998;	98US-0103328P.
PR	07-OCT-1998;	98US-0103395P.
PR	07-OCT-1998;	98US-0103396P.
PR	07-OCT-1998;	98US-0103401P.
PR	08-OCT-1998;	98US-0103633P.
PR	08-OCT-1998;	98US-0103678P.
PR	08-OCT-1998;	98US-0103679P.
PR	08-OCT-1998;	98US-0103711P.
PR	14-OCT-1998;	98US-0104257P.
PR	20-OCT-1998;	98US-0104987P.
PR	20-OCT-1998;	98US-0105000P.
PR	20-OCT-1998;	98US-0105002P.
PR	21-OCT-1998;	98US-0105104P.
PR	22-OCT-1998;	98US-0105169P.
PR	22-OCT-1998;	98US-0105266P.
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PR	26-OCT-1998;	98US-0105694P.
PR	27-OCT-1998;	98US-0105807P.
PR	27-OCT-1998;	98US-0105881P.
PR	27-OCT-1998;	98US-0105882P.
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PR	28-OCT-1998;	98US-0106023P.
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PR	28-OCT-1998;	98US-0106030P.
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PR	28-OCT-1998;	98US-0106178P.
PR	29-OCT-1998;	98US-0106248P.
PR	29-OCT-1998;	98US-0106384P.

PR	29-OCT-1998;	98US-0108500P.
PR	30-OCT-1998;	98US-0106464P.
PR	03-NOV-1998;	98US-0106856P.
PR	03-NOV-1998;	98US-0106902P.
PR	03-NOV-1998;	98US-0106905P.
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PR	03-NOV-1998;	98US-0106934P.
PR	10-NOV-1998;	98US-0107783P.
PR	17-NOV-1998;	98US-0108775P.
PR	17-NOV-1998;	98US-0108779P.
PR	17-NOV-1998;	98US-0108787P.
PR	17-NOV-1998;	98US-0108788P.
PR	17-NOV-1998;	98US-0108801P.
PR	17-NOV-1998;	98US-0108802P.
PR	17-NOV-1998;	98US-0108806P.
PR	17-NOV-1998;	98US-0108807P.
PR	17-NOV-1998;	98US-0108867P.
PR	17-NOV-1998;	98US-0108925P.
PR	18-NOV-1998;	98US-0108848P.
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PR	18-NOV-1998;	98US-0108850P.
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PR	18-NOV-1998;	98US-0108852P.
PR	18-NOV-1998;	98US-0108858P.
PR	18-NOV-1998;	98US-0108904P.
PR	22-DEC-1998;	98US-0113296P.
PR	30-DEC-1998;	98US-0114223P.
PR	05-JAN-1999;	99WO-US000106.
PR	16-APR-1999;	99US-0129674P.
PR	23-JUN-1999;	99US-0141037P.
PR	20-JUL-1999;	99US-0144758P.
PR	26-JUL-1999;	99US-0145698P.
PR	01-SEP-1999;	99WO-US020111.
PR	15-SEP-1999;	99WO-US021194.
PR	29-OCT-1999;	99US-0162506P.
PR	30-NOV-1999;	99WO-US028313.
PR	02-DEC-1999;	99WO-US028551.
PR	16-DEC-1999;	99WO-US030095.
PR	05-JAN-2000;	2000WO-US000219.
PR	06-JAN-2000;	2000WO-US000376.
PR	11-FEB-2000;	2000WO-US003565.
PR	18-FEB-2000;	2000WO-US004342.
PR	24-FEB-2000;	2000WO-US005004.
PR	02-MAR-2000;	2000WO-US005841.
PR	15-MAR-2000;	2000WO-US006884.
PR	17-MAY-2000;	2000WO-US013705.
PR	22-MAY-2000;	2000WO-US014042.
PR	30-MAY-2000;	2000WO-US014941.
PR	02-JUN-2000;	2000WO-US015264.
PR	23-AUG-2000;	2000WO-US023522.
PR	24-AUG-2000;	2000WO-US023328.
PR	08-NOV-2000;	2000WO-US030952.
PR	10-NOV-2000;	2000WO-US030873.
PR	01-DEC-2000;	2000WO-US032678.
PR	28-FEB-2001;	2001WO-US006520.
PR	01-MAR-2001;	2001WO-US006666.

PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;
 XX
 DR WPI; 2003-708344/67.
 DR N-PSDB; ADD70314.
 XX
 PT Novel isolated PRO polypeptide useful for tissue typing, modulating
 PT biological activity of cell, as molecular weight markers in protein
 PT electrophoresis, for treating arthritis, tumor.
 XX
 PS Claim 12; SEQ ID NO 277; 549pp; English.
 XX
 CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 4031; DB 7; Length 761;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG	60
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Qy	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKS	120
Db	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKS	120
Qy	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP	180
Db	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP	180
Qy	181	AHKHTAVLVDGMLYSGTMNIFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST	240
Db	181	AHKHTAVLVDGMLYSGTMNIFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST	240
Qy	241	QVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Db	241	QVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Qy	301	FNVRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Db	301	FNVRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Qy	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV	420
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Qy	421	ETAQGLDGHSHLVMYLGTTTGSLLHKAVVSGDSSAHLVEEIQLFDPDEPVVRNLQLAPTQGA	480

Db	421		ETAQGLDGHSHLVMYLGTTTGS	480
Qy	481	VFVGFSGGVWRVPRANCSVYES	540	
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Qy	541	GNPEWACASGPMRSRSLRPQSR	600	
Db	541	GNPEWACASGPMRSRSLRPQSR	600	
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Qy	661	VKVPLTRVSGGAALAAQQSYW	720	
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Qy	721	TLRPGEKAPLSREQHLQSPKE	761	
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OM protein - protein search, using sw model

Run on: May 5, 2004, 17:27:32 ; Search time 23 Seconds
(without alignments)
1708.146 Million cell updates/sec

Title: US-10-015-391A-277
Perfect score: 4031
Sequence: 1 MALPALGLDPWSLLGLFLFQ.....CRTSASDVADNNCLGTEVA 761

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1150.5	28.5	607	4	US-08-556-422A-4	Sequence 4, Appli
2	1044	25.9	862	4	US-08-556-422A-2	Sequence 2, Appli
3	825.5	20.5	771	1	US-08-121-713D-54	Sequence 54, Appl
4	825.5	20.5	771	1	US-08-835-268-54	Sequence 54, Appl
5	825.5	20.5	771	2	US-09-060-692-54	Sequence 54, Appl
6	825.5	20.5	771	3	US-08-833-391-54	Sequence 54, Appl
7	825.5	20.5	771	4	US-09-060-610-54	Sequence 54, Appl
8	825.5	20.5	771	5	PCT-US94-10151A-54	Sequence 54, Appl
9	815.5	20.2	655	4	US-08-556-422A-3	Sequence 3, Appli
10	709.5	17.6	775	4	US-09-308-179B-1	Sequence 1, Appli
11	699	17.3	425	4	US-08-556-422A-7	Sequence 7, Appli

12	673	16.7	888	4	US-09-077-940A-4	Sequence 4, Appli
13	672.5	16.7	887	4	US-09-077-940A-2	Sequence 2, Appli
14	666	16.5	1070	4	US-09-653-274-8	Sequence 8, Appli
15	666	16.5	1086	4	US-09-653-274-4	Sequence 4, Appli
16	655	16.2	641	4	US-09-653-274-13	Sequence 13, Appl
17	653.5	16.2	730	1	US-08-121-713D-58	Sequence 58, Appl
18	653.5	16.2	730	1	US-08-835-268-58	Sequence 58, Appl
19	653.5	16.2	730	2	US-09-060-692-58	Sequence 58, Appl
20	653.5	16.2	730	3	US-08-833-391-58	Sequence 58, Appl
21	653.5	16.2	730	4	US-09-060-610-58	Sequence 58, Appl
22	653.5	16.2	730	5	PCT-US94-10151A-58	Sequence 58, Appl
23	629	15.6	930	4	US-09-254-594-6	Sequence 6, Appli
24	615.5	15.3	536	4	US-09-653-274-10	Sequence 10, Appl
25	604	15.0	712	1	US-08-121-713D-64	Sequence 64, Appl
26	604	15.0	712	1	US-08-835-268-64	Sequence 64, Appl
27	604	15.0	712	2	US-09-060-692-64	Sequence 64, Appl
28	604	15.0	712	3	US-08-833-391-64	Sequence 64, Appl
29	604	15.0	712	4	US-09-060-610-64	Sequence 64, Appl
30	604	15.0	712	5	PCT-US94-10151A-64	Sequence 64, Appl
31	600.5	14.9	724	1	US-08-121-713D-62	Sequence 62, Appl
32	600.5	14.9	724	1	US-08-835-268-62	Sequence 62, Appl
33	600.5	14.9	724	2	US-09-060-692-62	Sequence 62, Appl
34	600.5	14.9	724	3	US-08-833-391-62	Sequence 62, Appl
35	600.5	14.9	724	4	US-09-060-610-62	Sequence 62, Appl
36	600.5	14.9	724	5	PCT-US94-10151A-62	Sequence 62, Appl
37	600	14.9	650	1	US-08-121-713D-60	Sequence 60, Appl
38	600	14.9	650	1	US-08-835-268-60	Sequence 60, Appl
39	600	14.9	650	2	US-09-060-692-60	Sequence 60, Appl
40	600	14.9	650	3	US-08-833-391-60	Sequence 60, Appl
41	600	14.9	650	4	US-09-060-610-60	Sequence 60, Appl
42	600	14.9	650	5	PCT-US94-10151A-60	Sequence 60, Appl
43	587	14.6	295	4	US-08-556-422A-6	Sequence 6, Appli
44	584	14.5	929	4	US-09-254-594-3	Sequence 3, Appli
45	526.5	13.1	477	1	US-08-136-922-2	Sequence 2, Appli

ALIGNMENTS

```

RESULT 1
US-08-556-422A-4
; Sequence 4, Application US/08556422A
; Patent No. 6576754
; GENERAL INFORMATION:
; APPLICANT: HALL, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim L.
; APPLICANT: BOUSSIOTIS, Vassiliki
; APPLICANT: NADLER, Lee M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DFN-005CPA2
; CURRENT APPLICATION NUMBER: US/08/556,422A
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 607

```

; TYPE: PRT
; ORGANISM: Mus musculus
US-08-556-422A-4

Query Match 28.5%; Score 1150.5; DB 4; Length 607;
Best Local Similarity 41.2%; Pred. No. 3.9e-106;
Matches 254; Conservative 103; Mismatches 215; Indels 45; Gaps 18;

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Qy      49 ERRALSFFHQKGLQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVP--RLKNMIPWPAS 106
      | | : | : : : | | | | | | | | | : | : : | : : : | |
Db      1 EERLIRKFEAENISNYTALLLSQDGKTLVVGAREALFALNSNLSFLPGGEYQELL-WSAD 59

Qy     107 DRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFASFPACTFIELQDSYLLPISE 166
      : | : | : | | : | | : | : | : | : | | | | | : | : |
Db      60 ADRKQQCSFKGKDPKRDCQNYIKILLPLNSSHLLTCGTAAFSPLCAYIHIASTLAQDEA 119

Qy     167 DKVM--EGKGQSPFDPAHKHTAVLVDGMLYSGTMNIFLGSEPILMRTLGSQPVLKTDNFL 224
      | : : | | | | | | | | | : | : | : | : | : | : | : |
Db     120 GNVILEDGKGHCPCFDPNFKSTALVVDGELYTGTVSSFQGNDAISRSQSSRPT-KTESSL 178

Qy     225 RWLHHDAFVAAIPSTQ-----VYFFFEETASEFDFFERLHTSRVARVCKNDVG 274
      | | | : | | : | : : | : | : | | | | | | | | | | | |
Db     179 NWL-QDPAFVASATSPESLGSPIGDDDKIYFFFSETGQEFEEFFENTIVSRVARVCKGDEG 237

Qy     275 GEKLLQKKWTTFLKAQLLCTQPGQ-LPFNVIRHAVLL---PADSPTAPHIYAVFTSQWQV 330
      | | : | | : | | : | | | | | | : | | | | : | | | | |
Db     238 GERVLQQRWTSFLKAQLLCSRPDGFPFNVLQDVFTLNPNPQDWRKTLSTI-GVFTSQWHR 296

Qy     331 GGTRSSAVCAFSLLDIERVFKGKYKELNKETSRTWTTYRGPETNPRPGSCSVGPS----- 384
      | | | | : | : : | : : | | | : | : | : | | | | | : |
Db     297 GTTEGSAICVFTMNDVQKAFDGLYKKVNRETQQWYTETHQVPTPRPGACITNSARERKIN 356

Qy     385 -----SDKALTFMKDHFMLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHS-HLVMYLG 438
      | : | | : | | | | | | | | | : : | : | | | | | : | : |
Db     357 SSLQLPDRVLNFLKDHFLMDGQVRSRLLLLQPRARYQRVAVHRVPGL--HSTDYDVLFLGT 414

Qy     439 TTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGAFFVGFSGGVWRVPRANCS 498
      | | | | | | | | | : | : | : | : | : | : | | | : | | |
Db     415 GDGRHLHKAVTL-SSRVHIIIEELQIFPQGPVQVQNLLLDHSHGGLLYASSHSGVVQVPVANC 473

Qy     499 VYESCVDCVLARDPHCAWDPESTRCCLLSAPNLS--WKQDMERGNPEWACASGPMRSRL 556
      : | : | | : | | | : | | | : | : | | | | | : | : |
Db     474 LYPTCGDCLLARDPYCAWTGSACRLASLYQPDLASRPWTQDIEGASVKELCKNSSYKARF 533

Qy     557 RPQSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAPPEASS--TVYNGSILLI- 613
      : | | : | | : : | | | | | : | | | | | : | : | : |
Db     534 LVPGKP--CKQVQIQPNTVNTLACPLLSNLATRLWVHNGAPVNASASCRVLPTGDLLLVG 591

Qy     614 VQDGVGGGLYQCWATENG 630
      | | : | : | | : | |
Db     592 SQQGL-GVFQCWSIEEG 607
```

RESULT 2
US-08-556-422A-2
; Sequence 2, Application US/08556422A
; Patent No. 6576754

```
; GENERAL INFORMATION:
; APPLICANT: HALL, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim L.
; APPLICANT: BOUSSIOTIS, Vassiliki
; APPLICANT: NADLER, Lee M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DFN-005CPA2
; CURRENT APPLICATION NUMBER: US/08/556,422A
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 862
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-556-422A-2
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Query Match          25.9%; Score 1044; DB 4; Length 862;
Best Local Similarity 35.2%; Pred. No. 3.4e-95;
Matches 271; Conservative 115; Mismatches 263; Indels 120; Gaps 27;
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Qy      38 PMPRVRYAGDERRALSF--FHQKGLQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVP 95
      |||: : | | : ||: : :: ||| | :|||:||||: |: : :
Db      26 PIPRITW----EHREVHLVQFHEPDIYNYSALLLSEDKDTLYIGAREAVFAVNALN--IS 79

Qy      96 RLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIE 155
      :: : | | : ||: || | || :|: | | :||| : | || ||| || ||| :
Db      80 EKQHEVYWKVSEDKKAKCAEKGKSKQTECLNYIRVLQPLSATSLYVCGTNAFQPACDHLN 139

Qy     156 LQDSYLLPISEDKVMEGKGQSPFDPAHKHTAVLVDGMLYSGTMNNFLGSEPILMRTLGSQ 215
      | | : || |||: ||||| :|:|: || |||| | ||||| : |
Db     140 LTSFKFLGKNED----GKGRCPFDPAHSYTSMVDGELYSGTSYNFLGSEPIISRNSSHS 195

Qy     216 PVLKTDNFLRWLHHDASFVAA-----IPST-----QVYFFFEETASEFDFFERLHTSRV 265
      | |:|: : || :: ||| | : | : |||| | : |:| | : | :
Db     196 P-LRTEYAIPLW-NEPSFVFADVIRKSPDSPDGEDDRVYFFFEVSVEYEFVFRVLIPRI 253

Qy     266 ARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQ-LPFNVIRHAVLLPADSPTAPHIYAVF 324
      |||| | || : |||||:||||:|:|:| | |||: | : | | :|
Db     254 ARVCKGDQGGLRTLQKKWTSFLKARLICSRPDSGLVFNVLRLDVFLRSPGLKVPVFYALF 313

Qy     325 TSQWQVGGTRSSAVCAFSLLDIERVFK-GKYKE---LNKETSRTWTTYRGPETNPRPGSCS 380
      | | : |||||:| | || ||| : : : :| | || | |||:|
Db     314 TP--QLNNVGLSAVCAYNLSTAEVFSHGKYMQSTTVEQSHTKWVRYNGFVVKPRPGACI 371

Qy     381 VGPS-----SDKALTFMKDHFMLDEQVV---GTPLLVKSGVEYTRLAVETAQGL 426
      : || | |:||| |||: | | |:| | ||:| : | |
Db     372 DSEARAANYTSSLNLPDKTLQFVKDHPMLDDSVTPIDNRPRLIKDKVNYTQIVVDRTQAL 431

Qy     427 DGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQG--AVFVG 484
      || : ||:| | |:||| :| : : |:| || ||| : | |: :| |: |
Db     432 DGSVYDVMFVSTDRGALHKA-ISLEHAVHIIETQLFQDFEPVQTL LLSKKGNRFVYAG 490

Qy     485 FSGGVWRVPRANC SVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPE 544
      : || : | | | : :| |||||: || | : || | |
Db     491 SNSGVVQAPLAFCGKHGTCEDCVLARDPYCAWSPPTATCVALHQTESPSRGLIQEMSGDA 550
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Qy 545 WACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPEASST 604
 | : : | | | : | : |
 Db 551 SVC-----PDKSKGSYRQHFFKHGGTAELKCSQKSNLARVFWKF-QNGVLKAESP 599
 Qy 605 VY-----NGSLLLVQDGVGGLYQCWATE---NGFSYPVISYWVDSQDQTLALDPELAGI 656
 | : : : | : | : | : : | : :
 Db 600 KYGLMGRKNLLIFNLSEGDSGVYQCLSEERVKNKTVFQVVAHV-----LEVKKV 649
 Qy 657 PREHVKVPLTRV-SGGAALAAQQSYWPHFVTVTVLFLVLSGALIILVAS-----PLRA 709
 | : | : : : : : : | | | |
 Db 650 PKPVVAPTLSVVQTEGSRIATK-----VLVASTQGSSPPTPA 686
 Qy 710 LRARGKVQGCETLRPGEKAP-----LSREQHLQSPKECRTSASD 748
 : : | | | : | : : : : :
 Db 687 VQATS--SGAITL-PPKPAPTGTSCPEKIVINTVPQLHSEKTMYLKSSD 732

RESULT 3

US-08-121-713D-54

; Sequence 54, Application US/08121713D

; Patent No. 5639856

; GENERAL INFORMATION:

; APPLICANT: Goodman, Corey S.

; APPLICANT: Kolodkin, Alex L.

; APPLICANT: Matthes, David

; APPLICANT: Bentley, David R.

; APPLICANT: O'Connor, Timothy

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 Bush Street, Suite 3200

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/121,713D

; FILING DATE: 13-SEP-1993

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Osman, Richard A.

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: B94-002-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415)343-4341

; TELEFAX: (415) 343-4342

; TELEX:

; INFORMATION FOR SEQ ID NO: 54:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 771 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-121-713D-54

Query Match 20.5%; Score 825.5; DB 1; Length 771;
Best Local Similarity 30.5%; Pred. No. 2.3e-73;
Matches 216; Conservative 119; Mismatches 282; Indels 91; Gaps 24;

Qy 35 GQGPMPRVRY-YAG--DERRALSFFHQKGLQDFDTLLLSGSGNTLYVGAREAILALDIQD 91
|: :||: | : :| : | | : : ||||: | : | :
Db 25 GKNNVPRLKLSYKEMLESNNVITFENGLANSSSYHTFLLDEERSRLYVGAKDHIFSFDLVN 84

Qy 92 PGVPRLKNM--IPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSP 149
:|: | | | : : | : | ||:| :| ||| ||| | |
Db 85 -----IKDFQKIVWPVSYTRDECKWAGKDILKECANFIKVLKAYNQTHLYACGTGAFHP 139

Qy 150 ACTFIEL---QDSYLLPISEDKVMGKGQSPFDPAHKHTAVLVDGMLYSGTMNNFLGSEP 206
||:|: : : : |:|:| : :|:| |||| :|:| :
Db 140 ICTYIEIGHHPEDNIFKLENSHFENGGRGKSPYDPKLLTASLLIDGELYSGTAADFMGRDF 199

Qy 207 ILMRTLGSQPVLKTDNF-LRWLHHDASFVAA-----IPSTQVVYFFFEETASEFDFFE 258
: ||| :|: | | :| :| :| | ||| | | : :
Db 200 AIFRTLGHHPIRTEQHDSRWL-NDPKFISAHLISESDNPEDDKVYFFFRENAIDGEHSG 258

Qy 259 RLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPG----QLPFNVIRHAVLLPADS 314
: :|: :||| | | : | |||||:|:| | | : : :|
Db 259 KATHARIGQICKNDFGGHRSVLNKWTTFLKARLICSVPGPNGIDTHFDELQDVFLMNFKD 318

Qy 315 PTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNP 374
| | :| ||| : : | ||| :| :| | | : :| :| |
Db 319 PKNPVVYGVFTTSSNI--FKGSAVCMYSMSDVRVFLGPYAHRDGPYQWVPYQGRVPYP 376

Qy 375 RPGSC-----SVGPS SDKALTFMKDHF LMDQV--GTPLLVKSGVEY--TRLAV 420
|||:| | :| :| :| | | | :|:| :| | :| :|
Db 377 RPGTCPSKTFGGFDSTKDLPPDVITFARSHPAMYNPVFPMNNRPIVIKTDVNYQFTQIVV 436

Qy 421 ETAQGLDGHSHLVMYLGTTTGSLHKAV-----VSGDSSAHLVEEIQLFPDPEPVRNLQLA 475
: || : ||:| | :| | | | :|:| :| :| : :|:
Db 437 DRVDAEDG-QYDVMFIGTDVGTVLKVVSI PKETWYDLEEV LLEEMTVFREPTAISAMELS 495

Qy 476 PTQGA VFGVGGVWRVPRANCSVY-ESCVCVLARDPHCAWD PESRTCCLLSAPNL--N 532
| :|:| : ||:| | :| :| :| | |||:| | :| |
Db 496 TKQQQLYIGSTAGVAQLPLHRCDIYGKACAECLARDPYCAWD---GSACSRYFPTAKRR 552

Qy 533 SWKQDMERGNPEWACAS--GPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASY 590
: :|:| :| | :| :| :| :| | | | | | |
Db 553 TRRQDIRNGDPLTHCSDLHHDNHHGHSPEER-----IIYGVENSSTFLECSPKSQRALVY 607

Qy 591 WS-----HGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDS 642
| :| :| :| :| :| :| :| :| :| :| :| :|
Db 608 WQFQRRNEERKEEIRVDDHII RTDQGLLLRS LQQKDSGNYLCHAVEHGFI----- 657

Qy 643 QDQTLALDPELAGIPREHVKVPLTRVSGG-----AALAAQQSYW 681
||| | | | ||:| :| | :| :| :| :| :| :|
Db 658 --QTL-LKVTLEVIDTEHLEELLHKDDDGDSKTKEMSNSMTPSQKVW 702

RESULT 4

US-08-835-268-54

; Sequence 54, Application US/08835268

; Patent No. 5807826

; GENERAL INFORMATION:

; APPLICANT: Goodman, Corey S.

; APPLICANT: Kolodkin, Alex L.

; APPLICANT: Matthes, David

; APPLICANT: Bentley, David R.

; APPLICANT: O'Connor, Timothy

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 Bush Street, Suite 3200

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/835,268

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/121,713

; FILING DATE: 13-SEP-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Osman, Richard A.

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: B94-002-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415)343-4341

; TELEFAX: (415) 343-4342

; TELEX:

; INFORMATION FOR SEQ ID NO: 54:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 771 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-835-268-54

Query Match 20.5%; Score 825.5; DB 1; Length 771;

Best Local Similarity 30.5%; Pred. No. 2.3e-73;

Matches 216; Conservative 119; Mismatches 282; Indels 91; Gaps 24;

Qy 35 GQGPMPRVRY-YAG--DERRALSFFHQKGLQDFDTLLLSGDGNTLYVGAREAILALDIQD 91

|: :||: | : :| : | | : : ||||: | : |: :

Db 25 GKNNVPRKLKLSYKEMLESNNVITFNGLANSSSYHTFLLDEERSRLYVGAKDHI FSFDLVN 84

Qy 92 PGVPRLKNM--IPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSP 149

```

      :|: | || | :| | : | :| ||:| | :| || | || | |
Db      85 -----IKDFQKIVVPVSYTRDECKWAGKDILKECANFIKVLKAYNQTHLYACGTGAFHP 139
Qy      150 ACTFIEL---QDSYLLPISEDKVMEGKGQSPFDPAHKHTAVLVDGMLYSGTMNFLGSEP 206
      ||:| |: : : : |:|:|:| |:|:| | | | |:| :
Db      140 ICTYIEIGHHPEDNIFKLENSHFENGGRGKSPYDPKLLTASLLIDGELYSGTAADFMGRDF 199
Qy      207 ILMRTLGSQPVLKTDNF-LRWLHHDASFVAA-----IPSTQVVYFFFEETASEFDFFE 258
      : | | | | :|:| | | | :| | | | | | | | | : :
Db      200 AIFRTLGHHPIRTEQHDRWL-NDPKFISAHLISESDNPEDDKVYFFFRENAIDGEHSG 258
Qy      259 RLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPG----QLPFNVIRHAVLLPADS 314
      : : |: :| | | | | : | | | | | |:|:| | | : : | :
Db      259 KATHARIGQICKNDFGGHRSVLNKWTTFLKARLICSVPGPNGIDTHFDELQDVFLMNFKD 318
Qy      315 PTAPHIYAVFTSQVQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNP 374
      | | :| | |: : : | | | |:| : | | | : : | | : | |
Db      319 PKNPVVYGVFTTSSNI--FKGSAVCMYSMSDVRVFLGPYAHRDGPYQWVPYQGRVPYP 376
Qy      375 RPGSC-----SVGPSSDKALTFMKDHFLMDEQVV---GTPLLKSGVEY--TRLAV 420
      ||:| | | | | :| | : | | | | | | | | | | | | |
Db      377 RPGTCPSKTFGGFDSTKDLRDDVITFARSHPAMYNPVFPMNNRPIVIKTDVNYQFTQIVV 436
Qy      421 ETAQGLDGHSHLVMYLGTTTGS LHKAV-----VSGDSSAHLVEEIQLFPDPEPVRNLQLA 475
      : | | : | |:| | | | | | | | | | | | | | | | |
Db      437 DRVDAEDG-QYDVMFIGTDVGTVLKVVSI PKETWYDLEEVLEEMTVFREPTAISAMELS 495
Qy      476 PTQGAVFVGFGSGGVWRVPRANCSVY-ESCVDCVLARDPHCAWDPESTRCCLLSAPNL--N 532
      | :|:| : | | :| | :| :| :| | | | | | | | : | |
Db      496 TKQQQLYIGSTAGVAQLPLHRCDIYGKACAECLLARDPYCAWD---GSACSRYPFTAKRR 552
Qy      533 SWKQDMERGNPEWACAS--GPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASY 590
      : |:| :| | | : | | | | | | | | | | | | | | |
Db      553 TRRQDIRNGDPLTHCSDLHHDNHHGHSPEER-----IIYGVENSSTFLECSPKSQRALVY 607
Qy      591 WS-----HGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDS 642
      | | | | | : | | | | | | | | | | | | | | | |
Db      608 WQFQRRNEERKEEIRVDDHIIRTDQGLLLRSLQQKDSGNYLCHAVEHGFI----- 657
Qy      643 QDQTLALDPELAGIPREHVKVPLTRVSGG-----AALAAQQSYW 681
      || | | | | | |:| : | | : : | | |
Db      658 --QTL-LKVTLEVIDTEHLEELLHKDDDGDSKTKEMSNSMTFSQKVW 702

```

RESULT 5

US-09-060-692-54

; Sequence 54, Application US/09060692

; Patent No. 5935865

; GENERAL INFORMATION:

; APPLICANT: Goodman, Corey S.

; APPLICANT: Kolodkin, Alex L.

; APPLICANT: Matthes, David

; APPLICANT: Bentley, David R.

; APPLICANT: O'Connor, Timothy

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:


```

; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-391-54

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Query Match          20.5%; Score 825.5; DB 3; Length 771;
Best Local Similarity 30.5%; Pred. No. 2.3e-73;
Matches 216; Conservative 119; Mismatches 282; Indels 91; Gaps 24;

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Qy      35 GQGPMPRVRY-YAG--DERRALSFFHQKGLQDFDFTLLLSGDGNTLYVGAREAILALDIQD 91
      |: :||: | : :| : | | : : ||||: | : |: :
Db      25 GKNVPRCLKLSYKEMLESNNVITFNGLANSSSYHTFLLDEERSRLYVGAKDHIFSFDLVN 84

Qy      92 PGVPRLKNN--IPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSP 149
      |: | | | :| : | : | | | :| | | | | | | | |
Db      85 -----IKDFQKIVWPVSYTRDECKWAGKDILKECANFIKVLKAYNQTHLYACGTGAFHP 139

Qy     150 ACTFIEL---QDSYLLPISEDKVMGKGQSPFDPAHKHTAVLVDGMLYSGMTMNNFLGSEP 206
      ||:|: : : : | :|:|:| :|:|:| | | | | :|:| :
Db     140 ICTYIEIGHHPEDNIFKLENSHFENGGRGKSPYDPKLLTASLLIDGELYSGTAADFMRDGF 199

Qy     207 ILMRTLGSQPVLKTDNF-LRWLHHDASFVAA-----IPSTQVVYFFFEETASEFDFFE 258
      : ||| :|: | | :| :| :| | | | | | | : :
Db     200 AIFRTLGHHPHPIRTEQHDNRWL-NDPKFISAHLISESDNPEDDKVYFFFRENAIDGEHSG 258

Qy     259 RLHTRSARVCKNDVGGKLLQKKWTTFLKAQLLCTQPG----QLPFNVIRHAVLLPADS 314
      : :|: :||| | | : | | | | | :|: | | : : | :
Db     259 KATHARIGQICKNDFGGHRSVLNKNWTTFLKARLICSVPGPNGIDTHFDELQDVFLMNFKD 318

Qy     315 PTAPHIYAVFTSQWQVGGRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNP 374
      | | :| ||| : : : ||| :|: | : ||| | | : : | :| |
Db     319 PKNPVVYGVFTTSSNI--FKGSAVCMYSMSDVRVRVFLGPYAHRDGPYQWVPYQGRVPYP 376

Qy     375 RPGSC-----SVGPSSDKALTFMKDHFMLDEQVV---GTPLLVKSGVEY--TRLAV 420
      ||:| | | :| :| :| | | | | :|:|: | | | :| :|
Db     377 RPTCPSKTFGGFDSTKDLPPDVITFARSHPAMYNPVFPMNNRPVIKTDVNYQFTQIVV 436

Qy     421 ETAQGLDGHSHLVMYLGTGTTGSLHKAV-----VSGDSSAHLVEEIQLFPDPEPVRNLQLA 475
      : | | : | :| | | :| :| | | | | :|:|: | : :|:|
Db     437 DRVDAEDG-QYDVMFIGTDVGTVLKVVSIPKETWYDLEEVLLLEEMTVFREPTAISAMELS 495

Qy     476 PTQGAVFVGFSGGVWRVPRANCSVY-ESCVDCVLARDPHCAWDPESTRCCLLSAPNL--N 532

```

Db	496	TKQQQLYIGSTAGVAQLPLHRCDIYGKACAECCCLARDPYCAWD---GSACSRYPFTAKRR	552
Qy	533	SWKQDMERGNPEWACAS--GPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASY	590
Db	553	TRRQDIRNGDPLTHCSDLHHDNHHGHSPEER-----IIYGVENSSTFLECSPKSQRALVY	607
Qy	591	WS-----HGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDS	642
Db	608	WQFQRRNEERKEEIRVDDHIIRTDQGLLLRSLQKDSGNYLCHAVEHGFI-----	657
Qy	643	QDQTLALDPELAGIPREHVKVPPLTRVSGG-----AALAAQQSYW	681
Db	658	--QTL-LKVTLEVIDTEHLEELLHKDDDDGSGSKTKEMSNSMTPSOKVW	702

RESULT 7

US-09-060-610-54

; Sequence 54, Application US/09060610

; Patent No. 6344544

; GENERAL INFORMATION:

; APPLICANT: Goodman, Corey S.

APPLICANT: Kolodkin, Alex L.

; APPLICANT: Matthes, David

; APPLICANT: Bentley, David R.

; APPLICANT: O'Connor, Timothy

; TITLE OF INVENTION: The Semaphorin Gene Family

```
; NUMBER OF SEQUENCES: 100
```

CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

```
; STREET: 268 Bush Street, Suite 3200
```

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

```
; MEDIUM TYPE: Floppy disk
```

```

;      COMPUTER:  IBM PC compatible

```

```
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
```

```
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

```

; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/09/060,610

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/835,268

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Osman, Richard A.

; REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: B94-002-1

; TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

; TELEFAX: (415) 343-4342

TELEX:

; INFORMATION FOR SEQ ID NO: 54:

; SEQUENCE CHARACTERISTICS:

```

;      LENGTH:  771 amino acids
;      TYPE:    amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-09-060-610-54

```

```

Query Match          20.5%;  Score 825.5;  DB 4;  Length 771;
Best Local Similarity 30.5%;  Pred. No. 2.3e-73;
Matches 216;  Conservative 119;  Mismatches 282;  Indels 91;  Gaps 24;

```

```

Qy      35 GQGPMPRVRY-YAG--DERRALSFFHQKGLQDFDTLLLSGSGDNTLYVGAREAILALDIQD 91
      | : : || : : | : : : : | : | : : || || : : | : : :
Db      25 GKNNVPRLKLSYKEMLESNNVITFENGLANSSSYHTFLLDEERSRLYVGAKDHIFSFDLVN 84

Qy      92 PGVPRLKNM--IPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSP 149
      : | : | | : : | : | : | | | : | | | | | | | |
Db      85 -----IKDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLKAYNQTHLYACGTGAFHP 139

Qy     150 ACTFIEL---QDSYLLPISEDKVMGKQSPFDPAHKHTAVLVDGMLYSGTMNNFLGSEP 206
      || : || : : : : | : : || : : | : | | | | : | : :
Db     140 ICTYIEIGHHPEDNIFKLENSHFENGGRKSPYDPKLLTASLLIDGELYSGTAADFMRGRDF 199

Qy     207 ILMRTLGSQPVLKTDNF-LRWLHHDASFVAA-----IPSTQVVYFFFEETASEFDFFE 258
      : | | | : : | : | | : | : | : | | | | | : : :
Db     200 AIFRTLGHHPHPIRTEQHDSRWL-NDPKFISAHLISESDNPEDDKVYFFFRENAIDGEHSG 258

Qy     259 RLHTSRVARVCKNDVGGKELLQKKWTTFLKAQLLCTQPG----QLPFNVIRHAVLLPADS 314
      : : : : || | | | : | | | | | | : : | : : : | :
Db     259 KATHARIGQICKNDFGGHRSVLNKWTTFLKARLICSVPGPNGIDTHFDELQDVFLMNFKD 318

Qy     315 PTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNP 374
      | | : | | | : : : | | | : : | : | | | : : : | : |
Db     319 PKNPVVYGVFTTSSNI--FKGSAVCMYSMSDVRVFLGPYAHRDGPYQWVPYQGRVPYP 376

Qy     375 RPGSC-----SVGPSSDKALTFMKDHFMLDEQVV---GTPLLKSGVEY--TRLAV 420
      || : | : | : | : | : | : | : | : | : | : | : |
Db     377 RPGTCPSKTFGGFDSTKDLRDDVITFARSHPAMYNPVFPMNNRPIVIKTDVNYQFTQIVV 436

Qy     421 ETAQGLDGHSHLVMYLGTTTGS LHKAV-----VSGDSSAHLVEEIQLFDPPEPVRNLQLA 475
      : | : | : || : | : : | : | : | : | : | : : : | :
Db     437 DRVDAEDG-QYDVMFIGTDVGTVLKVVSI PKETWYDLEEV LLEEMTVFREPTAISAMELS 495

Qy     476 PTQGAVFVGFSGGVWRVPRANCSVY-ESCVDCVLARDPHCAWDPESTRCCLLSAPNL--N 532
      | : : | : | : : | : | : : | : | | | : | : | : |
Db     496 TKQQQLYIGSTAGVAQLPLHRCDIYGKACAECCCLARDPYCAWD---GSACSRYFPTAKRR 552

Qy     533 SWKQDMERGNPEWACAS--GPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASY 590
      : : || : | : : | : | : | : | : | : | : | : |
Db     553 TRRQDIRNGDPLTHCSDLHHDNHHGHSPEER-----IIYGVENSSTFLECSPKSQRALVY 607

Qy     591 WS-----HGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDS 642
      | : : | : | : | : | : | : | : | : | : | : |
Db     608 WQFQRRNEERKEEIRVDDHIIRTDQGLLLRSLQQKDSGNYLCHAVEHGFI----- 657

Qy     643 QDQTLALDPELAGIPREHVKVPLTRVSGG-----AALAAQQSYW 681
      || | | | | || : : | : | : : | : |
Db     658 --QTL-LKVTLEVIDTEHLEELLHKDDDDGSGSKTKEMSNSMTPSQKVW 702

```

RESULT 8

PCT-US94-10151A-54

; Sequence 54, Application PC/TUS9410151A

; GENERAL INFORMATION:

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FLEHR HOHBACH TEST ALBRITTON & HERBERT

; STREET: 4 Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-4187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/10151A

; FILING DATE: 13-SEP-1994

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Osman, Richard A.

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: FP-58750-PC/RAO

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989

; TELEFAX: (415) 398-3249

; TELEX: 910 277299 FHT UR

; INFORMATION FOR SEQ ID NO: 54:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 771 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US94-10151A-54

Query Match 20.5%; Score 825.5; DB 5; Length 771;

Best Local Similarity 30.5%; Pred. No. 2.3e-73;

Matches 216; Conservative 119; Mismatches 282; Indels 91; Gaps 24;

```

Qy      35 GQGPMPRVRY-YAG--DERRALSFFHQKGLQDFDTLLLSGDGNTLYVGAREAILALDIQD 91
      |: :||:: | : :| : | | : : ||||:: | : |: :
Db      25 GKNNVPRCLKLSYKEMLESNNVITFNGLANSSSYHTFLLDEERSRLYVGAKDHIFSFDLVN 84

Qy      92 PGVPRLKNM---IPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSP 149
      |: | | | :| : | : | | | | :| | | | | | | | |
Db      85 -----IKDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLKAYNQTHLYACGTGAFHP 139

Qy     150 ACTFIEL---QDSYLLPISEDKVMEGKGQSPFDPAHKHTAVLVDGMLYSGTMNNFLGSEP 206
      ||::|: : : : |::|::| :::| | | | :|:| :
Db     140 ICTYIEIGHHPEDNIFKLENSHFENGRGKSPYDPKLLTASLLIDGELYSGTAADFMGRDF 199

```


US-08-556-422A-3

Query Match 20.2%; Score 815.5; DB 4; Length 655;
Best Local Similarity 31.3%; Pred. No. 1.8e-72;
Matches 203; Conservative 114; Mismatches 262; Indels 69; Gaps 21;

Qy 35 GQGPMPRVRY-YAG--DERRALSFFHQKGLQDFDTLLLSGDGNTLYVGAREAILALDIQD 91
|: :||: | : :| : | | : : ||||: | : | :
Db 25 GKNNVPRKLKLSYKEMLESNNVITFNGLANSSSYHTFLLDEERSRLYVGAKDHIFSFDLVN 84

Qy 92 PGVPRLKNM--IPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSP 149
:|: | | | : : | : | : | | : | | | | | | |
Db 85 -----IKDFQKIVWPVSYTRDECKWAGKDILKECANFIKVLKAYNQTHLYACGTGAFHP 139

Qy 150 ACTFIEL---QDSYLLPISEDKVMEGKGQSPFDPAHKHTAVLVDGMLYSGTMNNFLGSEP 206
||:|: : : : | : | : | : | : | : | : | :
Db 140 ICTYIEIGHHPEDNIFKLENSHFENGGRGKSPYDPKLLTASLLIDGELYSGTAAAFMGRDF 199

Qy 207 ILMRTLGSQPVLKTDNF-LRWLHHDASFVAA-----IPSTQVVYFFFEETASEFDFFE 258
: | | | : : | : | | : | : | : | | | | | : :
Db 200 AIFRTLGHHPIRTEQHDSRWL-NDPKFISAHLISESDNPEDDKVYFFFRENAIDGEHSG 258

Qy 259 RLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPG----QLPFNVIRHAVLLPADS 314
: : | : : | | | | | : | | | | | : | : | :
Db 259 KATHARIGQICKNDFGGHRSVLNKWTTFLKARLICSVPGPNGIDTHFDELQDVFLMNFKD 318

Qy 315 PTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNP 374
| | : | | | : : : | | | : | : | | | : : | : |
Db 319 PKNPVVYGVFTTSSNI--FKGSAVCMYSMSDVRVFLGPYAHRDGPYQWVPYQGRVPYP 376

Qy 375 RPGSC-----SVGPSSDKALTFMKDHFMLDEQVV---GTPLLKSGVEY--TRLAV 420
| | : | | : | : | : | : | : | : | : | : |
Db 377 RPGTCPSKTFGGFDSTKDLDDVITFARSHPAMYNPVFPMNNRPVVIKTDVNYQFTQIVV 436

Qy 421 ETAQGLDGHSHLVMYLGTTTGS LHKAV-----VSGDSSAHLVEEIQLFPDPEPVRNLQLA 475
: | | : | : | : | : | : | : | : | : | : : :
Db 437 DRVDAEDG-QYDVMFIGTVDVGTVLKVVSIKPTWYDLEEVLLLEMTVFREPTAISAMELS 495

Qy 476 PTQGAVFVGFGSGGVWRVPRANCSVY-ESCVDCVLARDPHCAWDPESTRCCLLSAPNL--N 532
| : : | : | : | : | : | : | : | : | : | : |
Db 496 TKQQQLYIGSTAGVAQLPLHRCDIYGKACAECCLARDPYCAWD---GSACSRYFPTAKRR 552

Qy 533 SWKQDMERGNPEWACAS--GPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASY 590
: : | : | : | : | : | : | : | : | : | : |
Db 553 TRRQDIRNGDPLTHCSDLHHDNHHGHSPEER-----IIYGVENSSTFLECSPKSQRALVY 607

Qy 591 WS-----HGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCWATENG 630
| : | : | : | : | : | : | : | : | : |
Db 608 WQFQRRNEERKEEI RVDHDIIRTDQGLLLRSLQQKDSGNYLCHAVEHG 655

RESULT 10

US-09-308-179B-1

; Sequence 1, Application US/09308179B

; Patent No. 6436669

; GENERAL INFORMATION:

; APPLICANT: INAGAKI, Shinobu

; APPLICANT: FURUYAMA, Tatsuo
 ; TITLE OF INVENTION: NOVEL SEMAPHORIN GENES (I)
 ; FILE REFERENCE: 0020-4562P
 ; CURRENT APPLICATION NUMBER: US/09/308,179B
 ; CURRENT FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: PCT/JP97/04111
 ; PRIOR FILING DATE: 1997-11-12
 ; PRIOR APPLICATION NUMBER: JAPAN 321068/1996
 ; PRIOR FILING DATE: 1996-11-15
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 775
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 US-09-308-179B-1

Query Match 17.6%; Score 709.5; DB 4; Length 775;
 Best Local Similarity 29.4%; Pred. No. 1e-61;
 Matches 214; Conservative 120; Mismatches 290; Indels 105; Gaps 31;

Qy	13	LLGLFLF-QLLQLLLPTTTAGGGGQGPMPRVRYAGD--ERRALSFFHQK-GLQDFDTLL	68
		: : :	
Db	7	ILTLLLWGHLLLELWTP----GHSANPSYPRRLRLSHKELLELNRTSIFQSPLGFLDLHTML	62
Qy	69	LSGDGNTLYVGAREAILALDIQDPGVPRLN---MI PWPASDRKKSECAFKKKSNETQCF	125
Db	63	LDEYQERLFGGRDLVYSLNLE-----RVSDGYREIYWPSTAVKVEECIMKGK-DANECA	116
Qy	126	NFIRVLVSYNVTHLYTCGTFAFSPACTFIEL---QDSYLLPISEDKVMGKGQSPFDPAH	182
		:	
Db	117	NYIRVLHHYNRTHLLTCATGAFDPHCAFIRVGHHSEEPFLHLESHRSEGRGRCPDPNS	176
Qy	183	KHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAA--IPST	240
		: : : : : : :	
Db	177	SFVSTLVGNELFAGLYSDYWGGRSAIFRSMGKLGHIRTEHDDERLLKEPKFVGSYMI PDN	236
Qy	241	Q-----VYFFFEETASEFDFFERLHT--SRVARVCKNDVGGEKLLQKKWTTFLKAQLLC	293
		:	
Db	237	EDRDDNKMYFFFTKALEAE--NNAHTIYTRVGRLCVNDMGGQRILVNKWSFTLKARLVC	294
Qy	294	TQPG----QLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERV	349
		:	
Db	295	SVPGMNGIDTYFDELEDVFLPTRDPKNPVI FGLFNTTSNI--FRGHAVCVYHMSSIREA	352
Qy	350	FKGKYKELNKETSRWTTYRGPETNPRPGSCS-----VGPSS---DKALTFMKDHFMD	399
Db	353	FNGPYAHKEGPEYHWSLYEGKVPYPRPGSCASKVNGGKYGTTKDYPDDAIRFARMHPLMY	412
Qy	400	EQVVGTT---PLLVKSGVEYT--RLAVETAQGLDGSHLVMYLGTTTGS LHKAVVSGDSSA	454
		: : : : : : :	
Db	413	QPIKPVHKKPILVKTDGKYNLRQLAVDRVEAEDG-QYDVLFIGTDTGIVLVKITIYNQET	471
Qy	455	H-----LVEEIQLFPDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRANCSVYES-CVDCVL	508
		:	
Db	472	EWMEEVILEELQIFKDPAPIISMEISSKRQQLYIGSASAVAQVRFHHCMDYGSACADCCCL	531

Qy 509 ARDPHCAWDPESTRCCLLSAP-----NLNSWKQDMERGNPEWAC-----ASGPMRSRLRP 558
 |||:|||| | | | :||: || | : |:
 Db 532 ARDPYCAWDGIS---CSRYYPYTGAAKRRFRQDVRHGNAQQCFGQQFVGDALDRT--- 585
 Qy 559 QSRPQIIKEVLAV---PNSILELPCPHLSALASYW--SHGPAAVPEASST-----VYN 607
 :| || || || | | | | | :
 Db 586 -----EERLAYGIESNSTL-LECTPRSLQAKVIFVQKGRDVRKEEVKTDDRVRVKMDL 637
 Qy 608 GSLLLVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGI-----PREHV 661
 | | | | : | | | : | : | : : : | : |
 Db 638 GLLFLVRKSDAGTYFCQTVEHNFVHTVRKITLE-----VVEEHKVEGMFHKDHEEERHH 692
 Qy 662 KVPLTRVSG 670
 | : | : | |
 Db 693 KMPCPPLSG 701

RESULT 11

US-08-556-422A-7

; Sequence 7, Application US/08556422A
 ; Patent No. 6576754
 ; GENERAL INFORMATION:
 ; APPLICANT: HALL, Kathryn T.
 ; APPLICANT: FREEMAN, Gordon J.
 ; APPLICANT: SCHULTZE, Joachim L.
 ; APPLICANT: BOUSSIOTIS, Vassiliki
 ; APPLICANT: NADLER, Lee M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
 ; FILE REFERENCE: DFN-005CPA2
 ; CURRENT APPLICATION NUMBER: US/08/556,422A
 ; CURRENT FILING DATE: 1995-11-09
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 425
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-08-556-422A-7

Query Match 17.3%; Score 699; DB 4; Length 425;
 Best Local Similarity 38.7%; Pred. No. 4.1e-61;
 Matches 167; Conservative 60; Mismatches 159; Indels 46; Gaps 13;

Qy 191 GMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAA-----IPST----- 240
 | ||||| |||||: | | | :|: : || : || | | :
 Db 1 GELYSGTSYNFLGSEPIISRNSSHSP-LRTEYAIPWL-NEPSFVFADVIRKSPDSPDGED 58
 Qy 241 QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQ-L 299
 ||||| | : |::| | : |::||| | | : |||||:||||:|::| |
 Db 59 DRVYFFFTVEVSVEYEFVFRVLIPRIARVCKGDQGLRTLQKKWTSFLKARLICSRPDSGL 118
 Qy 300 PFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFK-GKYKE-- 356
 |||:| : | : | ||:| | : ||||:| | || || :
 Db 119 VFNVLRDVFLRSPGLKVPVFYALEFTP--QLNNVGLSAVCAYNLSTAAEEVFSGHKYMQST 176
 Qy 357 -LNKETSRTTYRGPETNPRPGSCSVGPS-----SDKALTFMKDHFMDQVQV- 403
 : : :| | | | |||:| : || | |::||| | : |

Db 177 TVEQSHTKWVRYNGPVPKPRPGACIDSEARAANYTSSLNLPDKTLQFVKDHPLMDDSVTP 236

Qy 404 --GTPLLVKSGVEYTRLAVETAQGLDGHSHLVMYLGTGTTGSLHKAVVSGDSSAHLVEEIQ 461
 | : | | : : | : | | : | : : | : | | : | : : | : | |

Db 237 IDNRPRLIKVDNYTQIVVDRTQALDGTVDVFMFVSTDRGALHKA-ISLEHAVHIIETQ 295

Qy 462 LFPDPEPVRNLQLAPTQG--AVFVGFGSGVWRVPRANCSVYESCVDCVLARDPHCAWDPE 519
 | | | | : | : : | : | : | : | : | : | : | : | : |

Db 296 LFQDFEPVQTLILLSSKKGNRFVYAGSNSGVVQAPLAFCGKHGTCEDCVLARDPYCAWSPP 355

Qy 520 SRTCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELP 579
 : | | | | : | : | : | : | : | : | : | : | : |

Db 356 TATCVALHQTESPSRGLIQEMSGDASVC-----PDKSKGSYRQHFFKHGGTAELK 405

Qy 580 CPHLSALASYW 591
 | | | : |

Db 406 CSQKSNLARVFW 417

RESULT 12

US-09-077-940A-4

; Sequence 4, Application US/09077940A
 ; Patent No. 6576441
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMURA, Toru et al.
 ; TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE SAME
 ; FILE REFERENCE: 0020-4426P
 ; CURRENT APPLICATION NUMBER: US/09/077,940A
 ; CURRENT FILING DATE: 1998-06-05
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 888
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-077-940A-4

Query Match 16.7%; Score 673; DB 4; Length 888;
 Best Local Similarity 26.9%; Pred. No. 5.8e-58;
 Matches 210; Conservative 117; Mismatches 225; Indels 228; Gaps 32;

Qy 21 LLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQDFDTLLLSGDG----- 73
 | | | | | | | : | : | : | : |

Db 15 LLLLLL-----GGAHGLFP-----EDPPPLSVAPRDYLNHYPVFVGSGPGRLTPAEG 61

Qy 74 -----NTLYVGAREAILALDIQDPGVPRLK--NMIPWPASDRKKSECAFKKK 118
 | : | | : : : : | : : : | : : : | |

Db 62 ADDLNIQVRVLRVNRTLFIGDRDNLRYVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGK 121

Qy 119 SNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKQSPF 178
 | : | | : | : : | : | : | : | : | : | : | : |

Db 122 -QEGERNFVKVLLLRDESTLFVCGSNAPNPVCANYSIDT--LQPVGDN--ISGMARCPY 176

Qy 179 DPAHKHTAVLVDGMLYSGTMNFFLGSEPILMRTLGSQPVLKTDNFLRWLHHDAS----- 232
 | | | : | : | | : : | : : : | : | : | : |

Db 177 DPKHANVALFSDGMLFTATVTDFLAIDAVIYRSLGDRPTLRT-----VKHDSKWFKEPY 230

Matches 229; Conservative 132; Mismatches 291; Indels 195; Gaps 35;

```
Qy      18 LFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQDFDTLLLSGDG---- 73
      || || || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      14 LFLLLLLLRVT-----HGLFP-----DEPPPLSVAPRDYLSHYPVFVSGPGRLTP 59

Qy      74 -----NTLYVGAREAILALDIQDPGVP---RLKNMIPWPASDRKKSECA 114
      ||::| |: : ::: | | : : | :: |
Db      60 AEGAEDLNIQRLVRNRTLFIGDRDNLQVEL-EPSTSTELRYQRKLTWRSNPSDIDVCR 118

Qy     115 FKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKG 174
      | | | : | ||::||: : : | : ||: ||: | | : | | : : |
Db     119 MKGK-QEGECRNFKVLLLRDESTLFVCGSNAFNPICANYSMDTLQLLGDN----ISGMA 173

Qy     175 QSPFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLTNDNFRWLHHDAS-- 232
      : |::| | : | : |||:: | : : | | : :: |:: | | | : | | :
Db     174 RCPYDPKHANVALFSDGMLFTATVTDFLAIDAVIYRSLGDRPTLRT-----VKHDSKWF 227

Qy     233 ----FVAaipstQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGE-KLLQKKWTTFL 287
      || | : |||| | | ||:: |:: | ||||| ||||| : |::|::|
Db     228 KEPYFVHAVEWGSHVYFFFREIAMEFNYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFL 287

Qy     288 KAQLLCTQPG--QLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLD 345
      ||: | | : || ||:: || | | |||:: ||||| :
Db     288 KARLNCSPGDSHFYFNVLQ-AVTGVVSLGGRPVILAVFST--PSNSIPGSAVCAFDMNQ 344

Qy     346 IERVFKGKYKELNKETSRWTTYRGPE---TNPRPGSCSV-----GPSSDKALTFMKD 394
      : ||:|::: | || || |||| | : | | : |
Db     345 VAAVFEGRFREQKSPESIWTPV--PEDQVPRPRPGCCAAPGMQYNASNALPDEILNFVKT 402

Qy     395 HFLMDEQVVG---TPLLVKSGVEY--TRLAVETAQGLDGHSHLVMYLGTTTGS LHKAVVS 449
      | |||| | : | ::: : : ||:|: | | : : | :||: |:: | : |
Db     403 HPLMDEAVPSLGHSPIWVRTLIHQ LTRVAVDVGAGPWGNQTIV-FLGSEVGTVLKFLVK 461

Qy     450 GDSSAH-----LVEEIQLF-PD-----PEPVRNLQLAPTQGAVFVGFSGGVW 490
      ::| : || : : || : : : | | : | | |
Db     462 PNASVSGTTGPSIFLEEFETYRPDRCGRSSSAGEWGQRLLSLELDAASGGLLAAPRCVV 521

Qy     491 RVPRANCSVYESCV-DCVLARDPHCAWDPEsRTCCLLSAPNLNSWKQDMERGNPEWACAS 549
      ||| | | : | | : :|: :||: | | : : | | : ::|: :
Db     522 RVPVARCQLYSGCMKNCIGSQDPYCGWAPDG-SCI FLRPGTSATFEQDVSGASTSGLGDC 580

Qy     550 GPMSRSLRPQSRPQIIKEVLAVPNsILELPCPHLSALASYW----- 591
      : | : | :: | | : : : : | |
Db     581 TGLLRASLSDDRAGLVSVNLLVTSSVAAFVVGAVVSGFsvGWfVGLRERRELARRKDKEA 640

Qy     592 --SH-----GPAAVPEASSTVYNGSLLLIVQDGVGGL 621
      : | || || | : | : |
Db     641 ILAHGGSEAVLSVSRLGERRGTGTGGRGGAGGGPGGPPEA-----LLAPLMQNG---- 689

Qy     622 YQCW---ATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQ 678
      | | : | : | | || : :: : | | | |
Db     690 ---WTKAALLHGPHDL-----DSGLLPTPEQTPLPQK--RLPTTHPH---AHALGP 733

Qy     679 SYWPHFVTVTVLFALVLsGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQS 738
      | | | ||: || | | : : | | | | | :
Db     734 RAWDH-----SHALLSASASTSLLLLAHTRAPEQPPV-PTESGPESR---LCA 777
```

Qy 739 PKECRTS 745
|: || |
Db 778 PRSCRAS 784

RESULT 14

US-09-653-274-8

; Sequence 8, Application US/09653274
; Patent No. 6635742
; GENERAL INFORMATION:
; APPLICANT: Boyle, Bryan J
; APPLICANT: Yeung, George Y
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Mize, Nancy K
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Methods and Maaterials Relating to Semaphorin-Like
; TITLE OF INVENTION: Polypeptides and Polynucleotides
; FILE REFERENCE: HYS-23
; CURRENT APPLICATION NUMBER: US/09/653,274
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1070
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-653-274-8

Query Match 16.5%; Score 666; DB 4; Length 1070;
Best Local Similarity 29.1%; Pred. No. 4e-57;
Matches 206; Conservative 124; Mismatches 242; Indels 136; Gaps 35;

Qy 63 DFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIP-----WPASDRKKSECAFKK 117
|| :| | |||: |: : :: : :|: : :|| | : : : || |
Db 42 DFQIMLKIRD--TLYIAGRDQVYTVNLNE--MPKTE-VIPNKKLTWRSRQQDRENCAMKG 96

Qy 118 KSNETQCFNFIRVLVSYNVTHLYTCGTFASFSPACTFIELQD-SYLLPISEDKVMGKGQS 176
| :: :| |||:| | | :: ||| |||:| | : | : : : | :
Db 97 K-HKDECHNFIKVFVPRNDEMVFVCGTNAFNPFCRYRLSTLEY-----DGEEISGLARC 150

Qy 177 PFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNF-LRWLHHHDASFVA 235
||| : |: || ||| |: :|| |: : :|:| |:| : :|: : |: |
Db 151 PFDARQTNVALFADGKLYSATVADFLASDAVIYRSMGDGSALRTIKYDSKWI-KEPHFLH 209

Qy 236 AIPSTQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGG-EKLLQKKWTTFLKAQLLCT 294
|| ||||| | | : : |||||:||||:| : :|:| ||:||||:| | :
Db 210 AIEYGNVYVYFFFREIAVEHNNLGKAVYSRVARICKNDMGGSQRVLEKHWTSFLKARLNCS 269

Qy 295 QPGQ--LPFNVIRHAV-LLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFK 351
|| |:|: : : : | : |||: |: |||||: |||:| |
Db 270 VPGDPFFYFDVLQSITDIIQING--IPTVGVGFTT--QLNSIPGSAVCAFSMDIEKVKF 325

Qy 352 GKYKELNKETSRWTTYRGPE---TNPRPGSCSVGPSS-----DKALTFMKDHFILM 398
 |::|| | || || ||| |: : |: |:| | ||
 Db 326 GRFKEQKTPDSVWTAV--PEDKVPKPRPGCCAKHGLAEAYKTSIDFPDETLSFIKSHPLM 383
 Qy 399 DEQV---VGTPLLVKSGVEY--TRLAVETAQGLDGHSHLVMYLGTTTGS LHKAVVSGD-- 451
 | | | |: | | :|: : | : : |:|: | : | :
 Db 384 DSAVPPIADEPWFTKTRVRYRLTAISVDHSAG-PYQNYTVIFVGSEAGMVLKVLAKTSPF 442
 Qy 452 --SSAHLVEEIQLF-----PDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRANC SVY 500
 : : |:|:|: : : : | :|| |::| | : |:| : | |
 Db 443 SLNDSVLLLEEIEAYNHAKCSAENEEDKKVISLQLDKDHHALYVAFSSCIIRIPLSRCERY 502
 Qy 501 ESC-VDCVLARDPHCAWDPE SRTCCLLSAPNL-----NSWKQDMERGNPE 544
 || |: :|:|:| | |: | | : :|| | ||
 Db 503 GSCKKSCIASRDPYCGW--LSQGSCGRVTPGMLLLLTEDFFAFHNHSAEGYEQDTEFGN-- 558
 Qy 545 WACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPEASST 604
 | | : | : : | | :|: : : :|| :|| :
 Db 559 -TAHLGDCHEILPTSTTPDY--KIFGGPTSDMEVSSSSVTTMAS-----IPEITPK 606
 Qy 605 VYN-----GSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIP 657
 | : | :|| | : : | | || |:| ||
 Db 607 VIDTWRPKLTSSRKFFVQDD-----PNTSDFT---DP-LSGIP 640
 Qy 658 REHVKVPLTRVSGGAALAAQQSYWPHF-VTVTVLFLVLSGALIILVA 704
 | | | : : | | :|: : | | | ||
 Db 641 ----KGV RWEVQSG-----ESNQMVH MNVLITCVFAAFVLGAFIAGVA 679

RESULT 15

US-09-653-274-4

; Sequence 4, Application US/09653274

; Patent No. 6635742

; GENERAL INFORMATION:

; APPLICANT: Boyle, Bryan J

; APPLICANT: Yeung, George Y

; APPLICANT: Arterburn, Matthew C

; APPLICANT: Mize, Nancy K

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Drmanac, Radoje T

; TITLE OF INVENTION: Methods and Maaterials Relating to Semaphorin-Like

; TITLE OF INVENTION: Polypeptides and Polynucleotides

; FILE REFERENCE: HYS-23

; CURRENT APPLICATION NUMBER: US/09/653,274

; CURRENT FILING DATE: 2000-08-31

; PRIOR APPLICATION NUMBER: 09/491,404

; PRIOR FILING DATE: 2000-01-10

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 1086

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-653-274-4

Query Match

16.5%; Score 666; DB 4; Length 1086;

Best Local Similarity 29.1%; Pred. No. 4.1e-57;
Matches 206; Conservative 124; Mismatches 242; Indels 136; Gaps 35;

```

Qy      63 DFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIP-----WPASDRKKSECAFKK 117
      || :| | |||: |: : :: : :|: : :|| | : : : || |
Db      58 DFQLMLKIRD--TLYIAGRDQVYTVNLNE--MPKTE-VIPNKKLTWRSRQQDRENCAMKG 112

Qy     118 KSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQD-SYLLPISEDKVMEGKGQS 176
      | :: :| |||:| | | : : ||| ||:| | : | | : : : | :
Db     113 K-HKDECHNFIKVFVPRNDEMVFVCGTNAFNPMPCRYRLSTLEY-----DGEIISGLARC 166

Qy     177 PFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNF-LRWLHHDASFVA 235
      ||| : |: || ||| |: :|| |: :: |:| |:| : :|: : |:
Db     167 PFDARQTNVALFADGKLYSATVADFLASDAVIYRSMGDGSALRTIKYDSKWI-KEPHFLH 225

Qy     236 AIPSTQVVYFFFEETASEFDDFERLHTSRVARVCKNDVGG-EKLLQKKWTTFLKAQLLCT 294
      || |||| | | | : : |||||:||||:| :::|:| ||:||||:| |:
Db     226 AIEYGNVYVFFFREIAVEHNNLGKAVYSRVARICKNDMGGSQRVLEKHWTSLFKARLNCS 285

Qy     295 QPGQ--LPFNVIRHAV-LLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFK 351
      || |:|: : : : | : |||: |: |||||: |||:|
Db     286 VPGDPFFYFDVLQSITDIIQING--IPTVVGVFTT--QLNSIPGSAVCAFSMDDIEKVKF 341

Qy     352 GKYKELNKETSRWTTYRGPE---TNPRPGSCSVGPSS-----DKALTFMKDHFILM 398
      |:|:| | | | | || ||| |: : | : |:|:| | |
Db     342 GRFKEQKTPDSVWTAV--PEDKVPKPRPGCCAKHGLAEAYKTSIDFPDETLSFIKSHPLM 399

Qy     399 DEQV---VGTPLLKVGVEY--TRLAVETAQGLDGHSHLVMYLGTTTGS LHKAVVSGD-- 451
      | | | |: | | | ::|: : | : : |:|:| | : | :
Db     400 DSAVPPIADEPWFTKTRVRYRLTAISVDHSAG-PYQNYTVIFVGSEAGMVLKVLAKTSPF 458

Qy     452 --SSAHLVEEIQLF-----PDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRANCSVY 500
      : : |:|:|: : : : | :||| |:| || : |:| : | |
Db     459 SLNDSVLLLEEIEAYNHAKCSAENEEDKKVISLQLDKDHHALYVAFSSCIIRIPLSRCERY 518

Qy     501 ESC-VDCVLARDPHCAWDPESTRCCLLSAPNL-----NSWKQDMERGNPE 544
      || |: :|||:| | |: | | : :|| | ||
Db     519 GSCKKSCIASRDPYCGW--LSQGSCGRVTPGMLLLLTEDFFAFHNHSAEGYEQDTEFGN-- 574

Qy     545 WACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAPVEASST 604
      | | : | : : | | :|: : :|| :|| :
Db     575 -TAHLGDCHEILPTSTTPDY--KIFGGPTSDMEVSSSSVTMTAS-----IPEITPK 622

Qy     605 VYN-----GSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIP 657
      | : | :||| : :|| | || |:|
Db     623 VIDTWRPKLTSSRKFFVQDD-----PNTSDFT---DP-LSGIP 656

Qy     658 REHVKVPLTRVSGGAALAAQQSYWPHF-VTVTVLFALVLSGALIILVA 704
      | | | : : | | :| :|| : || | |
Db     657 ----KGVREWEVQSG-----ESNQMVHMNVLITCVFAAFVLGAFIAGVA 695

```

Search completed: May 5, 2004, 17:31:25
Job time : 26 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2004, 17:25:56 ; Search time 21 Seconds
(without alignments)
3485.798 Million cell updates/sec

Title: US-10-015-391A-277
Perfect score: 4031
Sequence: 1 MALPALGLDPWSLLGLFLFQ.....CRTSASDVDADNNCLGTEVA 761

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3280.5	81.4	760	2	I48745	semaphorin B - mou
2	1198.5	29.7	782	2	I48746	semaphorin C - mou
3	1079.5	26.8	834	2	S66498	M-sema F protein p
4	838.5	20.8	753	2	G02173	semaphorin III fam
5	838	20.8	772	2	A49069	collapsin - chicke
6	836	20.7	772	2	I48747	semaphorin D - mou
7	825.5	20.5	771	2	D49423	semaphorin III pre
8	820	20.3	749	2	G01856	semaphorin V - hum
9	802.5	19.9	751	2	I48748	semaphorin E - mou
10	784.5	19.5	748	2	I48744	semaphorin A - mou
11	766	19.0	666	2	I58169	semaphorin III - m
12	677.5	16.8	1074	2	JC5928	semaphorin F precu
13	657.5	16.3	730	2	JH0798	fasciclin IV precu

14	621.5	15.4	712	2	T27165	hypothetical prote
15	609.5	15.1	711	2	A49423	semaphorin I precu
16	605.5	15.0	656	2	B49423	semaphorin I - fru
17	600.5	14.9	724	2	C49423	semaphorin II prec
18	442.5	11.0	653	2	T03102	semaphorin homolog
19	350	8.7	676	2	T33853	hypothetical prote
20	281.5	7.0	1905	2	I51553	Plexin - African c
21	277	6.9	1872	2	JC4976	plexin 3 precursor
22	262	6.5	1894	2	JC4980	plexin 1 precursor
23	238	5.9	1884	2	JC4975	plexin 2 precursor
24	228	5.7	2051	2	T13164	plexin B - fruit f
25	225.5	5.6	1945	2	T13937	plexin A - fruit f
26	157	3.9	1806	2	T23298	hypothetical prote
27	151.5	3.8	1568	2	T09074	semaphorin recepto
28	146.5	3.6	403	2	E42521	A39R protein - vac
29	145	3.6	441	2	S29921	hypothetical prote
30	139.5	3.5	866	2	T06454	probable lipoxigen
31	132.5	3.3	317	2	T46426	hypothetical prote
32	132.5	3.3	1375	1	JC5148	hepatocyte growth
33	128.5	3.2	446	2	AI1253	glutathione reduct
34	127.5	3.2	1369	1	JC4860	protein-tyrosine k
35	127	3.2	1425	2	T30811	hepatocyte growth
36	121	3.0	1374	2	T30809	plasminogen relate
37	120	3.0	868	2	T06827	lipoxigenase (EC 1
38	119	3.0	1400	1	I38185	protein-tyrosine k
39	116	2.9	2126	2	H70621	probable polyketid
40	114	2.8	295	2	JQ1775	SalL9R protein - v
41	114	2.8	861	1	S01142	lipoxigenase (EC 1
42	114	2.8	862	2	T07775	lipoxigenase (EC 1
43	114	2.8	3573	2	S23070	erythronolide synt
44	112.5	2.8	862	2	S57964	lipoxigenase (EC 1
45	111.5	2.8	1378	1	I48751	protein-tyrosine k

ALIGNMENTS

RESULT 1

I48745

semaphorin B - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Nov-1999

C;Accession: I48745

R;Puschel, A.W.; Adams, R.H.; Betz, H.

Neuron 14, 941-948, 1995

A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates domains inhibitory for axonal extension.

A;Reference number: I48744; MUID:95267431; PMID:7748561

A;Accession: I48745

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-760 <RES>

A;Cross-references: EMBL:X85991; NID:g854325; PIDN:CAA59983.1; PID:g854326

C;Genetics:

A;Gene: semB

C;Superfamily: semaphorin

Query Match 81.4%; Score 3280.5; DB 2; Length 760;
Best Local Similarity 82.3%; Pred. No. 6.4e-252;
Matches 628; Conservative 46; Mismatches 84; Indels 5; Gaps 3;

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Qy      1 MALPALGLDPWSLLGLFLFQLLQILLPT--TTAGGGGQGPMRVRYYAGDERRALSFFHQ 58
      |||:| | | | | :| || | | | : | | | | | | | | | | | | | | | |
Db      1 MALPSLGQDSWSLLRVFFFQL--FLLPSLPASGTGGQGPMRVRKYHAGDGHRLSFFQQ 58

Qy     59 KGLQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMI PWPASDRKKSECAFKKK 118
      |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     59 KGLRDFDTLLLSDDGNTLYVGARETVLALNIQNPGIPRLKNMI PWPASERKKTECAFKKK 118

Qy    119 SNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPF 178
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    119 SNETQCFNFIRVLVSYNATHLYACGTFAFSPACTFIELQDSLLLPIIDKVMGKGQSPL 178

Qy    179 DPAHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIP 238
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    179 TLFTSTQAVLVDGMLYSGTMNFLGSEPILMRTLGSHPVLKTDIFLRWLHADASFVAAIP 238

Qy    239 STQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQ 298
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    239 STQVVYFFFEETASEFDFFEELYISRAVQVCKNDVGGEKLLQKKWTTFLKAQLLCAQPGQ 298

Qy    299 LPFNVIHAVLLPADSPTAPIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELN 358
      |||:| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    299 LPFNIIRHAVLLPADSPSVSRIYAVFTSQWQVGGTRSSAVCAFSLTDIERVFKGKYKELN 358

Qy    359 KETSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRL 418
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    359 KETSRWTTYRGSEVSPRPGSCSMGPSSDKALTFMKDHFMDHVVGTPLLVKSGVEYTRL 418

Qy    419 AVETAQGLDGHSHLVMYLGTTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQ 478
      |||:| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    419 AVESARGLDGSSHVMYLGSTGPLHKAVVPQDSSAYLVEEIQLSPDSEPVRNLQLAPAQ 478

Qy    479 GAVFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLSWKQDM 538
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    479 GAVFAGFSGGIWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCLSLSG-STKPWKQDM 537

Qy    539 ERGNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAV 598
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    538 ERGNPEWVCTRGPMAERSPRRQSPFQLIKEVLTVPNSILELRCPHLSALASYHWSHGRAKI 597

Qy    599 PEASSTVYNGSLLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPR 658
      |||:| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    598 SEASATVYNGSLLLLPQDGVGGLYQCVATENGYSYPVVSYWVDSQDQPLALDPELAGVPR 657

Qy    659 EHVKVPLTRVSGGAALAAQQSYWPHFVTVTVLFAVLVSGALIILVASPLRALRARGKVQG 718
      | | :| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    658 ERVQVPLTRVGGGASMAAQRSYWPHFLIVTVLLAIIVLLGVLTLLLASPLGALRARGKVQG 717

Qy    719 CETLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA 761
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    718 CGMLPPREKAPLSRDQHLQPSKDHRSTSASDVDADNNHLGAEVA 760
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RESULT 2

I48746

semaphorin C - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 03-Nov-2000

C;Accession: I48746

R;Puschel, A.W.; Adams, R.H.; Betz, H.

Neuron 14, 941-948, 1995

A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates domains inhibitory for axonal extension.

A;Reference number: I48744; MUID:95267431; PMID:7748561

A;Accession: I48746

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-782 <RES>

A;Cross-references: EMBL:X85992; NID:g854327; PIDN:CAA59984.1; PID:g854328

C;Genetics:

A;Gene: semC

C;Superfamily: semaphorin

Query Match 29.7%; Score 1198.5; DB 2; Length 782;
Best Local Similarity 39.9%; Pred. No. 1.1e-86;
Matches 275; Conservative 115; Mismatches 244; Indels 55; Gaps 22;

```

Qy      49 ERRALSFFHQKGLQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVP--RLKNMIPWPAS 106
      | | : | : : : | | | | | | | | | | : | : : : | |
Db      1 EERLIRKFEAENISNYTALLLSQDGKTLVVGAREALFALNSNLSFLPGGEYQELL-WSAD 59

Qy     107 DRKKSECAFKKKSNETQCENFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISE 166
      : | : | : | | : | | : | : | : | | | | | | : | : |
Db      60 ADRKQQCSFKGKDPKRDCQNYIKILLPLNSSHLLTCGTAAFSPLCAYIHIASTLAQDEA 119

Qy     167 DKVM--EGKGQSPFDPAHKHTAVLVDGMLYSGTMNPNFLGSEPIIMRTLGSQPVLKTDNFL 224
      | : : | | | | | | | | | | : | | : | : | : | | : |
Db     120 GNVILEDGKGHCPCFDPNFKSTALVVDGELYTGTVSSFGQNDPAISRSQSSRPT-KTESSL 178

Qy     225 RWLHHHDASFVAaipstQ-----VYFFFEETASEFDFFERLHTSRVARVCKNDVG 274
      | | | : | | : | : : : | | | | | | | | | | | | | |
Db     179 NWL-QDPAFVASATSPESLGSPIGDDDKIYFFFSETGQEFEEFFENTIVSRVARVCKGDEG 237

Qy     275 GEKLLQKKWTTFLKAQLLCTQPQG-LPFNVIRHAVLL---PADSPTAPHIYAVFTSQWQV 330
      | | : | | : | | : | | | | | | : | | | | : | | | | |
Db     238 GERVLQQRWTSFLKAQLLCSRPDGFPFNVLQDVFTLNPNPQDWRKTLSTI-GVFTSQWHR 296

Qy     331 GGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNPRPGSCSVGPS----- 384
      | | | | : | | : : | : : | | | : | : | : | | | | : |
Db     297 GTTEGSAICVFTMNDVQKAFDGLYKKVNRETQQWYTETHQVPTPRPGACITNSARERKIN 356

Qy     385 -----SDKALTFMKDHFMLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHS-HLVMYLGT 438
      | : | | : | | | | | | | | | | : : | | : | | | : | : |
Db     357 SSLQLPDRVLNFKLKHDFLMDGQVRSRLLLLQPRARYQRVAVHRVPGL--HSTYDVLFLGT 414

Qy     439 TTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRANCS 498
      | | | | | | | | : | : | : | : | : | : | | | : | | |
Db     415 GDGRLHKAVTL-SSRVHIIIEELQIFPQGPVQVQNLLLDSHGGLLYASSHSGVVQVPVANCS 473

Qy     499 VYESCVDCVLARDPHCAWDPEsRtCCLLSAPNLNS--WKQDMERGNPEWACASGPMSRSL 556

```

```

      :| :| ||:|||||:| | : | | | | | | : : | :
Db      474 LYPTCGDCLLARDPYCAWTGSACRLASLYQPDLASRPWTQDIEGASVKELCKNSSYKARF 533
Qy      557 RPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPEASS--TVYNGSLLLI- 613
      :| | :| ||: : | | | | | | : | | | | :| : | |||:
Db      534 LVPGKP--CKQVQIQPNTVNTLACPLLSNLATRLWVHNGAPVNASASCRVLPDGLLLVG 591
Qy      614 VQDGVGGGLYQCWATENGFSYPVISYWVDSQDQ-TLALDPELAGIPREHVKVPLTRVS--- 669
      | | : ||: ||| : | | | | | : : : | | | : |||
Db      592 SQQGL-GVFQCWSIEEGFQQLVASYCPEVMEEGVMDQKNQRDGTTP---VIINTSRVSAPA 647
Qy      670 -GGAALAAQQSYWPHFVTVTVL--FALVL 695
      | : | :||| | : : | ||:| |
Db      648 GGRDSWGADKSYWNEFLVMCTLFVFAMVL 676

```

RESULT 3

S66498

M-sema F protein precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 24-Nov-1999

C;Accession: S66498

R;Inagaki, S.; Furuyama, T.; Iwahashi, Y.

FEBS Lett. 370, 269-272, 1995

A;Title: Identification of a member of mouse semaphorin family.

A;Reference number: S66498; MUID:95385809; PMID:7656991

A;Accession: S66498

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-834 <INA>

A;Cross-references: EMBL:S79463; NID:g1110598; PIDN:AAB35184.1; PID:g1110599

C;Superfamily: semaphorin

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-834/Product: M-sema F protein #status predicted <MAT>

```

Query Match          26.8%; Score 1079.5; DB 2; Length 834;
Best Local Similarity 35.4%; Pred. No. 3.5e-77;
Matches 271; Conservative 115; Mismatches 242; Indels 137; Gaps 25;

```

```

Qy      39 MPRVRYIAGDERRALSFFHQKGLQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLK 98
      :|| :| : | | | | | | : | | | | | | :| : : | :
Db      28 VPRKTVSSGELVTVVRFSQTGIQDFLTTLTEHSGLLYVGAREALFAFSVE---ALELQ 84
Qy      99 NMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQD 158
      | | | | | | | | | | | | | | | | | | | | | | :
Db      85 GAISWEAPAEKKIECTQKGKSNQTECFNFIRFLQPYNSSHLYVCGTYAFQPKCTYINM-- 142
Qy     159 SYLLPISEDKVMGKGQSPFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVL 218
      : : : ||| : ||| | : ||| | | | : ||| | : ||| :
Db     143 -LTFTLDRAEFEDGKGKCPYDPAKGHTGLLVDGELYSATLNNFLGTPEVILRYMGTHHSI 201
Qy     219 KTDNFLRWLHHDASFV--AAIPST-----QVVYFFEETASEFDFFERLHTSRVARV 268
      || : | | : | | | : : : ||| | | | : | : : ||| |
Db     202 KTEYLAFWL-NEPHFVGSAFVPESVGSFTGDDDKIYFFFSERAVEYDCYSEQVVARVARV 260
Qy     269 CKNDVGGEKLLQKKWTTFLKAQLLCTQPG-QLPFNVIRHAVLLPADSPTAPHIYAVFTSQ 327
      || | : | | : ||| ||| ||| : ||| : | : | : | : :

```


Db	26	LPAT-----PRVR-----LSFKELKATGTAHFFNFLLNTTDYRILLKDEDH	66
Qy	74	NTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVS	133
Db	67	: : ::: : : : : : :: : :::	
Db	67	DRMYVGSKDYLSDLHD--INREPLIIHWAASPQRIEECVLSGKDVNGECGNFVRLIQP	124
Qy	134	YNVTHLYTCGTFAFSPACTFI----ELQDSYLLPISEDKVMGKQGQSPFDPAHKHTAVLV	189
Db	125	: : :: : : :: : : : :	
Db	125	WNRTHLYVCGTGAYNPMCTYVNRGRRAQD-YIFYLEPERLESGKGKCPYDPKLDTASALI	183
Qy	190	DGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNF-LRWLHHDDASFVAA--IPST----QV	242
Db	184	: : : : : : : : : : :	
Db	184	NEELYAGVYIDFMGTDAAI FRTL GKQTAMRTDQYNSRWL-NDPSFIHAELIPDSAENDDK	242
Qy	243	VYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPG----Q	298
Db	243	: :: :: : : : : : : : :	
Db	243	LYFFFRERSAEAPQSPAVY-ARIGRICLNDDGGHCCLVNKWSFTFLKARLVCSVPGEDGIE	301
Qy	299	LFPNVIRHAVLLPADSPTAPIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELN	358
Db	302	: :: : : :	
Db	302	THFDELQDVVFVQQTQDVRNPVIYAVFTSSGSV--FRGSAVCVYSMADIRMVFNPGPFAPKE	359
Qy	359	KETSRWTTYRGPETNPRPGSCSVG---PS-----SDKALTFMKDHFMLDEQVV---GT	405
Db	360	: : : : : : :	
Db	360	GPNYQWMPFSGKMPYPRPGTCPPGGTFTPSMKSTKDYPDEVINFMRSHPLMYQAVYPLQRR	419
Qy	406	PLLVKSGVEY--TRLAVETAQGLDGHSHLVMYLGTTTGS LHKAVV---SGDSSAHLVEE	459
Db	420	: :: : : : : :: : : :	
Db	420	PLVVRTGAPYRLTTIAVDQVDSADGR-YEVLF LGTDRGTQKVIVLPKDDQEMEELMLEE	478
Qy	460	IQLFPDPPEPVRNLQLAPTQGA VFVGFSGGVWRVPRANCSVY-ESCVDCVLARDPHCAWDP	518
Db	479	:: : : : : : : : :	
Db	479	VEVFKDPAPVKMTTIS SKRQQLYVASAVGVTHLSLHRCQAYGAACADCCCLARDPYCAWD-	537
Qy	519	ESRTCCLLSAPN-LNSWKQDMERGNPEWACASGPMSRSLRPQSRPQIIKEV-LAVPNSIL	576
Db	538	: : : : : : : : :	
Db	538	-GQACSRYTASSKRRSRQDVRHGNPIRQC-----RGFNSNANKNAVESVQYGVAGSAA	590
Qy	577	ELPCPHLSALASYW--SHGPA-----AVPEASSTVYNGSLLLIVQDGVGGLYQCWATE	628
Db	591	: : : : :	
Db	591	FLECQPRSPQATVKWLFQRDPGDRRREIRAEDRFLRTEQGLLLRALQLSDRGLYSC TATE	650
Qy	629	NGFSYPV--ISYWVDSQDQT-LALDPEL--AGIPREHVKVPLTRVSGGAALAAQ-----	677
Db	651	: : : :	
Db	651	NNFKHVTRVQLHLVLGRDAVHAALFPPLSMSAPPPGAGPPTPPYQELAQLLAQPEVGLI	710
Qy	678	----QSYWPH 683	
Db	711		
Db	711	HOYCOGYWRH 720	

RESULT 5

collapsin - chicken

C;Date: 07-Apr-1994 #sequence revision 07-Apr-1994 #text change 24-Sep-1999

C;Accession: A49069

R;Luo, Y.; Raible, D.; Raper, J.A.

Cell 75, 217-227, 1993

A;Title: Collapsin: a protein in brain that induces the collapse and paralysis of neuronal growth cones.

A;Reference number: A49069; MUID:94006554; PMID:8402908

A;Accession: A49069

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-772 <LUO>

A;Cross-references: GB:U02528; NID:g410078; PIDN:AAC59638.1; PID:g410079

C;Superfamily: semaphorin

Query Match 20.8%; Score 838; DB 2; Length 772;

Best Local Similarity 31.6%; Pred. No. 4.6e-58;

Matches 203; Conservative 120; Mismatches 256; Indels 64; Gaps 19;

```
Qy      39 MPRVRYAGDERRALSFFHQKGL---QDFDTLLLSGDGNTLYVGAREAILALDIQDPGVP 95
      :||::      :      : : : ||      : | || : : |||||:: | : :: :
Db      29 VPRKLKSYKEMLESNNIVNFENGLANSSSYHTFLLDEERSRLYVGAKDHIFSFLNVN---- 84

Qy      96 RLK--NMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTF 153
      :|      | || | : : || : |      :| |||::|| :|| |||| ||| || | ||:
Db      85 -IKEYQKIVWPVSHSRDECKWAGKDILRECANFIKVLKTYNQTHLYACGTGAFHMPCTY 143

Qy     154 IEL---QDSYLLPISEDKVMEGKGQSPFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMR 210
      ||:      :      : :      |:|:|:|:|      :||| | |||| :|:| : : |
Db     144 IEVGSHPEDNIFRMEDSHFENGGRGKSPYDPKLLTASLLVDGELYSGTAADFMGRDFAIFR 203

Qy     211 TLGSQPVLKTDNF-LRWLHHDASFVAA-----IPSTQVVYFFFEETASEDFDFFERLHT 262
      |||      ::|:      ||| :| |:|      |      :||| | | : : :
Db     204 TLGHHHPIRTEQHDSRWL-NDPRFISAHLPESDNPEDDKIYFFFRENAIDGEHTGKATH 262

Qy     263 SRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPG----QLPFNVIRHAVLLPADSPTAP 318
      :|: :||| | | : | |||||::|:|: ||      |: :: | : : | |
Db     263 ARIGQICKNDFGGHRSVLNKWTTFLKARLICSVPGPNGIDTHFDELQDVFLMNSKDKPNP 322

Qy     319 HIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNPRPGS 378
      :| |||:      :      : ||| |:| :| || | | :      :| |:| |||:
Db     323 IVYGVFTTSSNI--FKGSAVCMYSMTDVRRVFLGPYAHRDGPNYQWVPYQGRVPYPRPGT 380

Qy     379 C-----SVGPSSDKALTFMKDHFMLDEQVV---GTPLLVKSGVEY--TRLAVETAQ 424
      |      |      |: :|| : | | |      |::|: |:| |:| |:
Db     381 CPSKTFGGFDSTKDLPEVITFARSHPAMYNPVFPINSRPIMIKTVDYQFTQIVVDRVD 440

Qy     425 GLDGHSHLVMYLGTTTGSLHKAVVSGDSSAH-----LVEEIQLFDPPEPVRNLQLAPTQG 479
      || : ||::|| |:| | |      : |      |:|: :| :| : ::: |
Db     441 AEDG-QYDVMFIGTDIGTVLKVVSIPKETWHELEEVLLLEEMTVFREPTVISAMKISTKQQ 499

Qy     480 AVFVGFGSGGVWRVPRANCSVY-ESCVCVLARDPHCAWDPESTRCCLLSAPNL--NSWKQ 536
      ::| : | | ::| | || :| :| ||||:| || | |      : :|
Db     500 QLYIGSATGVSQQLPLHRCDVYGKACAECLARDPYCAWDGSS---CSRYFPTAKRRTRRQ 556

Qy     537 DMERGNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHG-- 594
      |: |:| |:      :      | :      | : | || | | | | ||
Db     557 DIRNGDPLTHCSD--LQHHDNPSGQTLEEKIIYGVENSSTFLECSPKSQRAIVYWQFQKQ 614

Qy     595 -----PAAVPEASSTVYNGSLLLIVQDGVGGGLYQCWATENG 631
```


Db 615 NDDHKVEIKVDDRMIRTEQGLLLRSLQRRDSGIYFCHAVEHGF 657

RESULT 6

I48747

semaphorin D - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999

C;Accession: I48747

R;Puschel, A.W.; Adams, R.H.; Betz, H.

Neuron 14, 941-948, 1995

A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates domains inhibitory for axonal extension.

A;Reference number: I48744; MUID:95267431; PMID:7748561

A;Accession: I48747

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-772 <RES>

A;Cross-references: EMBL:X85993; NID:g854329; PIDN:CAA59985.1; PID:g854330

C;Genetics:

A;Gene: semD

C;Superfamily: semaphorin

Query Match 20.7%; Score 836; DB 2; Length 772;
Best Local Similarity 30.3%; Pred. No. 6.6e-58;
Matches 220; Conservative 124; Mismatches 279; Indels 102; Gaps 25;

Qy	24	LLLPTTTAGGGGQGPMPVRVY-YAG--DERRALSFFHQKGLQDFDTLLLSGDGNTLYVGA	80
		: : : : : : : :	
Db	14	VLLTARANYANGKNNVPRKLKSYKEMLESNNVITFNGLANSSSYHTFLLDEERSRLVGA	73
Qy	81	REAILALDIQDPGVPRKLN--IPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTH	138
		:: : :: : : : : : : : : : :	
Db	74	KDHIFSFNLVN-----IKDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLEAYNQTH	128
Qy	139	LYTCGTFAFSPACTFIEL---QDSYLLPISEDKVMGKGQSPFDPAHKHTAVLVDGMLYS	195
		: : : : : : : : : :	
Db	129	LYACGTGAFHPICTYIEVGHHPEDNIFKLQDSHFENGRGKSPYDPKLLTASLLIDGELYS	188
Qy	196	GTMNNFLGSEPILMRTLGSQPVLKTDNF-LRWLHHDAFVAA-----IPSTQVVYFFF	247
		: : : : : : :	
Db	189	GTAADFMRDFAIFRTLGDHHPITREQHDSRWL-NDPRFISAHLPESDNPEDDKVYFFF	247
Qy	248	EETASEFDFFERLHTRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPG----QLPFNV	303
		: : : : : : : :	
Db	248	RENAIGGEHSGKATHARIGQICKNDFGGHRSVLNKWTTFLKARLICSVPGPNGIDTHFDE	307
Qy	304	IRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSR	363
		:: : : : : : : : : : :	
Db	308	LQDVFLMNSKDPKNPIVYGVFTTSSNI--FKGSACVMSMSDVRVFLGPYAHRDGPYQ	365
Qy	364	WTTYRGPETNPRPGSC-----SVGPSSDKALTFMKDHFLMDEQVV---GTPLL VKS	411
		: : : : : :	
Db	366	WVPYQGRVPYPRPGTCPSKTFGGFDSTKDLDDVITFGRSHPAMYNPVPINNRPIMIKT	425
Qy	412	GVEY--TRLAVETAQGLDGHSHLVMYLGTTGSLHKAVVSGDSSAH-----LVEEIQLFP	464

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      | | | : : | :      | | : | : : | | | : : | :      | : | : : |
Db      426 DVNYQFTQIVVDRVDAEDG-QYDVMFIGTVDGTVLKVVSVPKETWHDLEEVLLEEMTVFR 484

Qy      465 DPEPVRNLQLAPTQGAVFVGFSGGVWRVPRANCSVY-ESCVDCVLARDPHCAWDPESTRC 523
      : | : : : | : : : | : | : : | : | : : | : | : : | : |
Db      485 EPTTISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECCLARDPYCAWDGSS--- 541

Qy      524 CLLSAPNL--NSWKQDMERGNPEWACAS-----GPMRSRLRPQSRPQIIKEVLAVPN 573
      | | | : : | : | : | : | : | : | : | : | : | : | : |
Db      542 CSRYFPTAKRRTRRQDIRNGDPLTHCSDLEDHDNHHGP---SLEE-----RIIYGVEN 591

Qy      574 SILELPCPHLSALASYW-----SHGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCW 625
      | | | | | | | | : : | : | : | : | : | : | : |
Db      592 SSTFLECSPKSQRALVYWQFQRRNRSSKREIRMGDHIIRTEQGLLLRSLQKKDSGNYLCH 651

Qy      626 ATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGG-----AALAA 676
      | | : | | | | | | | : : | : | : : | : : : :
Db      652 AVEHGFM-----QTL-LKVTLEVIDTEHLEELLHKDDGDGSGKIKEMSSSMTP 698

Qy      677 QQSYW 681
      | |
Db      699 SQKVV 703

```

RESULT 7

D49423

semaphorin III precursor - human

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999

C;Accession: D49423

R;Kolodkin, A.L.; Matthes, D.J.; Goodman, C.S.

Cell 75, 1389-1399, 1993

A;Title: The Semaphorin genes encode a family of transmembrane and secreted growth cone guidance molecules.

A;Reference number: A49423; MUID:94094332; PMID:8269517

A;Accession: D49423

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-771 <KOL>

A;Cross-references: GB:L26081; NID:g799328; PIDN:AAA65938.1; PID:g436560

C;Genetics:

A;Gene: GDB:SEMA1

A;Cross-references: GDB:283448

C;Superfamily: semaphorin

```

Query Match          20.5%;  Score 825.5;  DB 2;  Length 771;
Best Local Similarity 30.5%;  Pred. No. 4.5e-57;
Matches 216;  Conservative 119;  Mismatches 282;  Indels 91;  Gaps 24;

```

```

Qy      35 GQGPMPRVRY-YAG--DERRALSFFHQKGLQDFDTLLLSGDGNTLYVGAREAILALDIQD 91
      | : : | : : | : : : | : : : | : : : | : : : | : : :
Db      25 GKNNVPRLKLSYKEMLESNNVITFNGLANSSSYHTFLLDDEERSRLYVGAKDHIFSFDLVN 84

Qy      92 PGVPRLKNM--IPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSP 149
      : | : | | : : | : : | : | : | : | : | : | : |
Db      85 -----IKDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLKAYNQTHLYACGTGAFHP 139

```

Qy 150 ACTFIEL---QDSYLLPISEDKVMGKQSPFDPAHKHTAVLVDGMLYSGTMNNFLGSEP 206
 ||:||: : : : ||:||: || :||: ||||| :||: :
 Db 140 ICTYIEIGHHPEDNIFKLENSHFENGGRKSPYDPKLLTASLLIDGELYSGTAADFMGRDF 199

Qy 207 ILMRTLGSQPVLKTDNF-LRWLHHDASFVAA-----IPSTQVVYFFFEETASEFDFFE 258
 : |||| :||: ||| :| |::| | |||| | | : :
 Db 200 AIFRTLGHHPHPIRTEQHDSRWL-NDPKFISAHLISESDNPEDDKVYFFFRENAIDGEHSG 258

Qy 259 RLHTSRVARVCKNDVGGKELLQKKWTTFLKAQLLCTQPG---QLPFNVIRHAVLLPADS 314
 : :||: |||| || : | ||||| ||:||: || | : : | :
 Db 259 KATHARIGQICKNDFGGHRSVLNKWTTFLKARLICSVPGPNGIDTHFDELQDVFLMNFKD 318

Qy 315 PTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRTWTTYRGPETNP 374
 | | :| ||| : : : |||| :| : ||| | | : : | :| |
 Db 319 PKNPVVYGVFTTSSNI--FKGSAVCMYSMSDVRVFLGPYAHRDGPYQWVPYQGRVPYP 376

Qy 375 RPGSC-----SVGPSSDKALTFMKDHFMLDEQVV---GTPLLVKSGVEY--TRLAV 420
 |||:| | | :|| : | | | | :||: | | | :|
 Db 377 RPGTCPSKTFGGFDSTKDLDPDDVITFARSHPAMYNPVFPMNNRPIVIKTDVNYQFTQIVV 436

Qy 421 ETAQGLDGHSHLVMYLGTGTTGSLHKAV-----VSGDSSAHLVEEIQLFPDPEPVRNLQLA 475
 : || : ||: || | :| | | | :||: :| :| : :||:
 Db 437 DRVDAEDG-QYDVMFIGTDVGTVLKVVSI PKETWYDLEEVLL EEMTVFREPTAISAMELS 495

Qy 476 PTQGAVFVGFGSGGVWRVPRANCSVY-ESCVDCVLARDPHCAWDPESTRCCLLSAPNL--N 532
 | :|| : || :|| | :| :|| :| ||||: |||| : | |
 Db 496 TKQQQLYIGSTAGVAQLPLHRCDIYGKACAECC LARDPYCAWD---GSACSRYPFTAKRR 552

Qy 533 SWKQDMERGNPEWACAS--GPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASY 590
 : :||: | :| | : | : | : | | | | | | |
 Db 553 TRRQDIRNGDPLTHCSDLHHDNHHGHSPEER-----IIYGVENSSTFLECSPKSQRALVY 607

Qy 591 WS-----HGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDS 642
 | | : | || :| | | | | :||
 Db 608 WQFQRRNEERKEEIRVDDHIIRTDQGLLLRSLQKDSGNYLCHAVEHGF----- 657

Qy 643 QDQTLALDPELAGIPREHVKVPLTRVSGG-----AALAAQQSYW 681
 ||| | | | ||: | : | : : | |
 Db 658 --QTL-LKVTLEVIDTEHLEELLHKDDDDGDGSKTKEMSNSMTPSQKVW 702

RESULT 8

G01856

semaphorin V - human

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Sep-1999

C;Accession: G01856

R;Sekido, Y.

submitted to the EMBL Data Library, June 1995

A;Reference number: G08634

A;Accession: G01856

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-749 <SEK>

A;Cross-references: EMBL:U28369; NID:g974283; PIDN:AAD09138.1; PID:g974284

C;Superfamily: semaphorin

Query Match 20.3%; Score 820; DB 2; Length 749;
 Best Local Similarity 31.2%; Pred. No. 1.2e-56;
 Matches 207; Conservative 116; Mismatches 254; Indels 86; Gaps 24;

```

Qy      32 GGGGQGMPRVRYAGDERRALSF-----FHQKGLQDF-----DTLLLSGDGNTLYV 78
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      20 GLGSAAPSP-----PRLRLSFQELQAWH--GLQTFSLERTCCYQALLVDEERGRFLV 69

Qy      79 GAREAILALDIQDPGVPRLNMI PWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTH 138
      || : : : : : : : : : : : : : : : : : : : : : : : :
Db      70 GAENHVASLNLDN--ISKRAKKLAWPAPVEWREECNWAGKDIGTECMNFVKLLHAYNRTH 127

Qy     139 LYTCGTFAFSPACTFIEL---QDSYLLPISEDKVMGKGQSPFPDPAHKHTAVLVDGMLYS 195
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     128 LLACGTGAFHPTCAFVEVGHRAEEPVLRLDPGRIEDGKGKSPYDPRHRAASVLVGEELYS 187

Qy     196 GTMNNFLGSEPILMRTLGSQPVLKTD-NFLRWLHHDA SFVAI-----PSTQVVYFFF 247
      | : : : : : | | | | | | | | | | | | | | | | | | | |
Db     188 GVAADLMGRDFTIFRSLGQRPSLRTEPHDSRWL-NEPKFVKVFWIPESENPDDDKIYFFF 246

Qy     248 EETASE-FDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQP---GQLPFNV 303
      || | | | | | | | | | | | | | | | | | | | | | | | |
Db     247 RETAVEAAPALGRLSVSRVGQICRNDVGGQ RSLVNKWTTF LKARLVCSVPGVGEDTHFDQ 306

Qy     304 IRHAVLLPADSPTAPHIYAVFTSQWQVGGRSSAVCAFSLLDIERVFKGKYKELNKETSR 363
      : : | | : | : | | | | : : : | | | : | : | : | : :
Db     307 LQDVFLSSRDHRTPLLYAVFSTSSSI--FQGSAVCVYSMNDVRR AFLGPF AHKEGPMHQ 364

Qy     364 WTTYRG PETNPRPGSC-----SVGPSSDKALTFMKDHF LMD EQVV---GTPLLVKS 411
      | : | : | | | | | | | | | | | | | | | | | | | | | |
Db     365 WVS YQGRVPYPRPGMCP SKTFGTFSSTKDFPDDVIQFARNHPLMYNSVLPTGGRPLFLQV 424

Qy     412 GVEY--TRLAVETAQGLDGHSHLVMYLGTTTGS LHK--AVVSG---DSSAHLVEEIQLFP 464
      | | | : : : | | | : | : : | | | : | | : | : | : |
Db     425 GANYTFTQIAADRVAADGH-YDVLFIGTDVGTVLKVISVPKGSRPSAEGLLLEELHVFE 483

Qy     465 DPEPVRNLQLAPTQGAVFVGFSGGVWRVPRANCSVY-ESCVDCVLARDPHCAWD PESRTC 523
      | | | : : : : : : | : : | : : | : | | | | | | | |
Db     484 DSAAVTSMQISSKRHQLYVASRSAVAQIALHRC AAHGRVCTECC LARDPYCAWD---GVA 540

Qy     524 CLLSAPNLNS--WKQDMERGNPEWACASGPM SRSRLRPQSRPQIIK-EVLAVPNSILELPC 580
      | | | : : : | : | | : | | | : : : | | | | | | | |
Db     541 CTRFQPSAKRRFR RQDVRNGDPSTLCSG-----DSSRPALLEHKVFGVEGSSAFLEC 592

Qy     581 PHL SALASYW-----SHGPAAVPEASSTVYNGSLL LVLIVQDGVGGGLYQCWATENGFS 632
      | | | | : | | : | | | : : | | | | | | | | | |
Db     593 EPRSLQARVEWTFQ RAGVTAHTQVLAEERTERTARGLLLRLRLRRRDSGVYLCAAVEQGFT 652

Qy     633 YPV 635
      | :
Db     653 QPL 655
  
```

RESULT 9
 I48748
 semaphorin E - mouse
 C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
 C;Accession: I48748
 R;Puschel, A.W.; Adams, R.H.; Betz, H.
 Neuron 14, 941-948, 1995
 A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates domains inhibitory for axonal extension.
 A;Reference number: I48744; MUID:95267431; PMID:7748561
 A;Accession: I48748
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-751 <RES>
 A;Cross-references: EMBL:X85994; NID:g854331; PIDN:CAA59986.1; PID:g854332
 C;Genetics:
 A;Gene: semE
 C;Superfamily: semaphorin

Query Match 19.9%; Score 802.5; DB 2; Length 751;
 Best Local Similarity 31.2%; Pred. No. 2.9e-55;
 Matches 219; Conservative 119; Mismatches 264; Indels 101; Gaps 26;

Qy	13	LLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRA-----LSFFHQKGLQDFDT	66
		: : : :	
Db	9	LVGVFICSI-----CVRGSSQPQARV-YLTFDELRETKTSEYFSLSHQQ--LDYRI	56
Qy	67	LLLSGDGNTLYVGAREAILALDIQDPGVPRLNMI PWPASDRKKSECAFKKKSNETQCFN	126
		: : : : : : : : :	
Db	57	LLMDEDQDRIYVGSKDHILSLNINNISQEPLS--VFWPASTIKVEECKMAGKDPTHGCCN	114
Qy	127	FIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVM-----EGKGQSPFD	179
		: : : : : :	
Db	115	FVRVIQTFNRTHLYVCGSGAFSPVCTYLNRRGR-----SEDQVFMIDSKCESGKGRCSFN	169
Qy	180	PAHKHTAVLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNF-LRWLHH----DASFV	234
		: : : : : : : : : : : : : :	
Db	170	PNVNTVSMINEELFSGMYIDFMGTDAAFRSLTKRMQLRTDQHNSKWLSEPMFVDAHVI	229
Qy	235	--AAIPSTQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLL	292
		: : : : : : : :	
Db	230	PDGTDPNDAKVYFFFKERLTDNNRSTKQIHSMIARICPNDTGGQSRSLVNKWTTFLKARLV	289
Qy	293	CT---QPG-QLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGRSSAVCAFSLLDIER	348
		: : : : : : : : : : :	
Db	290	CSVTEDEGPETHFDELEDVFLLETDPRTTLVYGIFTTSSSV--FKGSAVCVYHLSDIQT	347
Qy	349	VFKGKYKELNKETSRWTTYRGPETNPRPGSCSVGPSS-----DKALTFMKDHFILM	398
		: : : : : : :	
Db	348	VFNGPFAHKEGPNHQLISYQGRIPIYPRPGTCPGGAFTPNMRTTKDFPDDVVTFIRNHPLM	407
Qy	399	DEQVV---GTPLLVKSGVE--YTRLAVETAQGLDGHSHLVMYLGTTTGS LHKAVV----S	449
		: : : : : : : : : :	
Db	408	YNSISPIHRRPLIVRIGTDYKYTKIAVDRVNAADGRYH-VLFLGTDGRGTQKVVLPTNS	466
Qy	450	GDSSAHLVEEIQLFPDEPVRNLQLAPTQGAVFVGFGGVRVPRANCSVY-ESCVD CVL	508
		: : : : : : : : : : : : :	
Db	467	SASGELILEELEVFKNHVPITTM EISSKKQQLYVSSNEGVSQVSLHRCHIYGTACADCCCL	526
Qy	509	ARDPHCAWDPE SRTCCLLSAP--NLNSWKQDMERGNPEWACASGPMSRSLRPQSRPQIIK	566

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      |||:|||| | | | | :||: ||| | : : :|::
Db      527 ARDPYCAWDGHS---CSRFYPTGKRRSRRQDVRHGNPLTQCRGFENLKAY---RNAAEIVQ 580
Qy      567 EVLAVPNSILELPCPHLSALASYW-----SHGPAAVPEASSTVYNGSLLLIVQDGVG 619
      | |: | | | | | | | : | | | | ||
Db      581 --YGVRRNSTFLECAPKSPQASIKWLLQKDKDRRKEGKLNERIIATSQGLLIRSVQDSDQ 638
Qy      620 GLYQCWATENGFSYPVISYWVDSQDQTLA-----LDPELAGI 656
      ||| | |||| | | | | ||:| | | |: :
Db      639 GLYHCIATENSFK-----QTIAKINFKVLDSEMVAV 669

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RESULT 10

I48744

semaphorin A - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999

C;Accession: I48744

R;Puschel, A.W.; Adams, R.H.; Betz, H.

Neuron 14, 941-948, 1995

A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates domains inhibitory for axonal extension.

A;Reference number: I48744; MUID:95267431; PMID:7748561

A;Accession: I48744

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-748 <RES>

A;Cross-references: EMBL:X85990; NID:g854323; PIDN:CAA59982.1; PID:g854324

C;Genetics:

A;Gene: sema

C;Superfamily: semaphorin

```

Query Match          19.5%; Score 784.5; DB 2; Length 748;
Best Local Similarity 31.1%; Pred. No. 7.7e-54;
Matches 210; Conservative 117; Mismatches 281; Indels 67; Gaps 23;

```

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Qy      31 AGGGGQGP-MPRVR--YYAGDERRALSFFHQKGLQDFDTLLLSGDGNTLYVGAREAILAL 87
      || | | :||:| : | : | : : ||: : |:|| : :|
Db      19 AGLGDTAPNLPRLRLSFQELQARHGVRTFRLERTCCYEALLVDEERGRLFVGAENHVASL 78
Qy      88 DIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAF 147
      : : : : : ||| : || : | |:| ||:|:| :|| ||| | | ||
Db      79 SLDN--ISKRAKKLAWPAPVEWREECNWAGKDIGTECMNFVRLHAYNHTLLACRTGAF 136
Qy      148 SPACTFIELQDSYLLPIS--EDKVMGKQGQSPFDPAHKHTAVLVDGMLYSGTMNNFLGSE 205
      | | : | :|: :|||:|:| | : :||| |||| : :| :
Db      137 HPTCALWRWATAGGTHASTGPEKLEDGKGKTPYDPRHRPPSVLVGEELYSGVTADLMGRD 196
Qy      206 PILMRTLGSQPVLKTD-NFLRWLHHDSAFVAI-----PSTQVVYFFFEETASE-FDF 256
      : |:|| | |:|: : ||| : : | | : |||| |:| |
Db      197 FTIFRSLGQNPSLRTEPHDSRWL-NEPKFVKVFWIPESENPDDDKIYFFFRSAVEAAPA 255
Qy      257 FERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQP---GQLPFNVIRHAVLLPAD 313
      |: ||| :|:|:|:|:| | |||||:|:|:| | | |: : : || :
Db      256 MGRMSVSRVGQICRNDLGGQSRSLVNKWTTFLLKARLVCSVPGVEGDTHFDQLQDVFLSSR 315
Qy      314 SPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETN 373

```

```

      | :|||:: | : ||| :|: |: | | | | :| :|:|
Db      316 DRQTPLLYAVFST--SSGVFQGSACVYSMNDVRRRAFLGPLPHKEGPTHQWVS YQGRVPY 373
Qy      374 PRPGSC-----SVGPSSDKALTFMKDHFILMDEQVV---GTPLLVKSGVEY--TRLA 419
      ||| | | : | :| | | : | | :| | | :|
Db      374 PRPGMCPSKTFGTFSSTKDFPDDVIQFGRNHPLMYPVLPMGGRPLFLQVGAGYTFTQIA 433
Qy      420 VETAQGLDGHSHLVMYLGTTTGSLHK--AVVSG---DSSAHLVEEIQLFDPPEPVRNLQL 474
      : ||| : |::|| |:: | : | :| |::|:| | : ::|
Db      434 ADRVAAADGH-YDVLFIGTDTVGLKVISVPKGRPNSEGLLLEELQVFEDSAAITSMQI 492
Qy      475 APTQGAVFVGFSGGVWRVPRANCSVY-ESCVDCLARDPHCAWDPESTRCCLLSAPNLNS 533
      : : ::| |:: | : :| :| |::|:| | : | |
Db      493 SSKRQQLYVASRAAVAQIALHRCTALGRACAECCLARDPYCAWD---GSACTRFQPTAKR 549
Qy      534 --WKQDMERGNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYW 591
      :||: |:| | | | |: : |::| : | | | |
Db      550 RFRRQDIRNGDPSTLC-SGDSSHV-----LLEKKVLGVESGSAFLECEPRSLQAHVQW 602
Qy      592 -----SHGPAAVPEASSTVYNGSLLLVQDGVGGLYQCWATENGFSYP----VISYW 639
      :| | | | | :| :| | | | | | | :
Db      603 TFQGAGEAAHTQVLAEEVERTARGLLLRRLQDSGVYLCVAVEQGFSQLRRLVLHVL 662
Qy      640 VDSQDQTLALDPELA 654
      :| : || | |
Db      663 SAAQAERLARAEEAA 677

```

RESULT 11

I58169

semaphorin III - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Sep-1999

C;Accession: I58169

R;Messersmith, E.K.; Leonardo, E.D.; Shatz, C.J.; Tessier-Lavigne, M.; Goodman, C.S.; Kolodkin, A.L.

Neuron 14, 949-959, 1995

A;Title: Semaphorin III can function as a selective chemorepellent to pattern sensory projections in the spinal cord.

A;Reference number: I58169; MUID:95267432; PMID:7748562

A;Accession: I58169

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-666 <RES>

A;Cross-references: GB:L40484; NID:g703189; PIDN:AAA73934.1; PID:g703190

C;Genetics:

A;Gene: SemaIII

C;Superfamily: semaphorin

Query Match 19.0%; Score 766; DB 2; Length 666;

Best Local Similarity 31.4%; Pred. No. 1.9e-52;

Matches 195; Conservative 102; Mismatches 232; Indels 92; Gaps 21;

```

Qy      123 QCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIEL---QDSYLLPISEDKVMEGKGQSPFD 179
      :| |||:| | | ||| || | | | :|:| : : : | :|:|:|
Db      7 ECANFIKVLEAYNQTHLYACGTGAFHPICITYIEVGHPEDNIFKLQDSHFENGGRGKSPYD 66

```

QY 180 PAHKHTAVLVDGMLYSGTMNNFLGSEPIILMRTLGSQPVLKTDNF-LRWLHHDASFVAA-- 236
 | : : : | | | | | : : : | | | : : : | | : : | : : |
 Db 67 PKLLTASLLIDGELYSGTAAANFMGRDFAIFRTLGHHPHPIRTEQHDSRWL-NDPRFISAHL 125

QY 237 -----IPSTQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQL 291
 | | | | | | : : : : : : : : | | : | | | | | : |
 Db 126 IPESDNPEDDKVYFFFRENAIDGEHSGKATHARIGQICKNDFGGHRSVLNKTWTTFLKARL 185

QY 292 LCTQPG----QLPFNVIRHAVLLPADSPTAPIYAVFTSQWQVGGTRSSAVCAFSLLDIE 347
 : : | | : : : | : : | | : : : | | : : : | : : | : : |
 Db 186 ICSVPGPNGIDTHFDELQDVFLMNSKDPKNPIVYGVFTTSSNI--FKGSAVCMYMSDVR 243

QY 348 RVFKGKYKELNKETSRWTTYRGPETNPRPGSC-----SVGPSSDKALTFMKDHFILM 398
 | | | : : : | : | | | : | | : | : | : | : | : | : |
 Db 244 RVLLGPYAHRDGPYQWVPYQGRVPYPRPGTCPSKTFGGFDSTKDLRDDVITFARSHPAM 303

QY 399 DEQVV---GTPLLVKSGVEY--TRLAVETAQGLDGSHLVMYLGTGSLHKAVVSGDSS 453
 | : : : | | : : : | : : : | : : : | : : : | : : : | : : : |
 Db 304 YNPVFPINNRPIMIKTDVNYQFTQIVVDRVDAEDG-QYDVMFIGTDVGTVLKVVSVPKET 362

QY 454 AH-----LVEEIQLFDPPEPVRNLQLAPTQGAVFVGFGSGGVWRVPRANCSVY-ESCVDVCV 507
 | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
 Db 363 WHDLEEVLLLEMTVFREPTTISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECC 422

QY 508 LARDPHCAWDPESTRCCLLSAPNL--NSWKQDMERGNPEWACAS-----GPMSRSLR 557
 | | | : | | | : : : : | : : : : | : : : : | : : : : | : : : : |
 Db 423 LARDPYCAWDGSS---CSRYFPTAKRRTRRQDIRNGDPLTHCSDLQHHDNHHGP---SLE 476

QY 558 PQSRPQIIKEVLAVPNSILELPCPHLSALASYWS-----HGPAAVPEASSTVYNGS 609
 : : | | | | | | | | : : : : : | : : : : | : : : : | : : : : |
 Db 477 E-----RIIYGVENSSTFLECSPKSQRALVYWQFQRRNEDRKEEIKMGDHIIRTEQGL 529

QY 610 LLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVS 669
 | | : | | | | : | | | | | | | | | | | | : : : : | : : : : |
 Db 530 LLRSLQKKDSGNYLCHAVEHGFM-----QTL-LKVTLEVIDTEHLEELLHKDD 576

QY 670 GG-----AALAAQQSYW 681
 | : : : | | : : : | : : : | : : : | : : : | : : : | : : : |
 Db 577 DGDGSKIEMSSSMTSPSQKVW 597

RESULT 12

JC5928

semaphorin F precursor - human

C;Species: Homo sapiens (man)

C;Date: 10-Apr-1998 #sequence_revision 08-May-1998 #text_change 17-Nov-2000

C;Accession: JC5928

R;Simmons, A.D.; Pueschel, A.W.; McPherson, J.D.; Overhauser, J.; Lovett, M. Biochem. Biophys. Res. Commun. 242, 685-691, 1998

A;Title: Molecular cloning and mapping of human semaphorin F from the Cri-du-chat candidate interval.

A;Reference number: JC5928; MUID:98125554; PMID:9464278

A;Accession: JC5928

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1074 <SIM>

A;Cross-references: GB:U52840; NID:g2772583; PIDN:AAC09473.1; PID:g2772584

C;Accession: JH0798
 R;Kolodkin, A.; Matthes, D.J.; O'Connor, T.P.; Patel, N.H.; Admon, A.; Bentley, D.; Goodman, C.S.
 Neuron 9, 831-845, 1992
 A;Title: Fasciclin IV: Sequence, expression, and function during growth cone guidance in the grasshopper embryo.
 A;Reference number: JH0798; MUID:93040225; PMID:1418998
 A;Accession: JH0798
 A;Molecule type: mRNA
 A;Residues: 1-730 <KOL>
 A;Cross-references: GB:L00709; NID:g160844; PID:g160845
 A;Experimental source: embryo
 C;Comment: This protein plays a role in growth cone guidance in the developing central nervous system.
 C;Keywords: glycoprotein; transmembrane protein
 F;1-22/Domain: signal sequence #status predicted <SIG>
 F;23-730/Product: fasciclin IV #status predicted <MAT>
 F;23-627/Domain: extracellular #status predicted <EXT>
 F;628-652/Domain: transmembrane #status predicted <TMM>
 F;653-730/Domain: intracellular #status predicted <INT>
 F;44,71,163,267,360,539/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.3%; Score 657.5; DB 2; Length 730;
 Best Local Similarity 29.5%; Pred. No. 8.9e-44;
 Matches 213; Conservative 115; Mismatches 246; Indels 149; Gaps 34;

Qy	41	RVRYAGDERRALSFFHQGLQDFDTLLSGDGNTRYVVGAREAILALDIQDPGVPRLKNM	100
		: : : : : : : :	
Db	37	RVQRFGLGNESHKDH-----KLEKDHNSLLVGARNIVYNISLRDL-TEFTEQR	84
Qy	101	IPWPASDRKKSECAFKKKSNETQCENFIRVLVSYNVTHLYTCGTFASFSPACTFIELQD-S	159
		: : : : : :	
Db	85	IEWHSSGAHRELCYLKGKS-EDDCQNYIRVLAKIDDDRVLICGTNAYKPLCRHYALKDGD	143
Qy	160	YLLPISEDKVMGKQSPFDPAHKHTAVLVDGMLYSGTMNFLGSEPIMLRTLGSQPVLK	219
		: : : : : : : : : :	
Db	144	YV-----EKEYEGRGLCPFDPDNHSTAIYSEGLYSATVADEFSGTDPLIYR-----GPLRT	195
Qy	220	TDNFLRWLHHDAFVAAPSTQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLL	279
		: : : : : : : : : :	
Db	196	ERSDLKQL-NAPNFVNTMEYNDFIFFFFRETAVEYINCGKAIYSRVARVCKHDKGGPHQF	254
Qy	280	QKKWTTFLKAQLLCTQPGQLP--FNVIRHAVLLPAD-----SPTAPHIYAVFTSQWQV	330
		: : : : : : : : : :	
Db	255	GDRWTSFLKSRLNCSVPGDYPPFYFNEIQST----SDIIEGNYGGQVEKLIYGVFTT--PV	308
Qy	331	GGRSSAVCAFSLLDIERVFKGKYKELNKETSRW---TTRYGPETNPRPGSCSVGPS---	384
		: : : :	
Db	309	NSIGGSAVCAFSMKSIKESFDGPFKEQETMNSNWLAVPSLVPE--PRPGQC-VNDSRTL	365
Qy	385	SDKALTFMKDHFLMDEQVVG---TPLLVKSGVEY--TRLAV-ETAQGLDGSHLVMYLGT	438
		: : : : : : : : : : : : : : :	
Db	366	PDVSVNFVKSHTLMDAEPFAFFTRPILIRISLQYRFTKIAVDQQVVRTPDGKAYDVLFIGT	425
Qy	439	TTGSLHKAV--VSGDSS---AHLVEEIQLFDPPEPVRNLQLAPTQG--AVFVGFSGG--	488
		: : : : : : : : : :	

Db 426 DDGKVIKALNSASFSSDTVDSVVIEELQVLPPGVPVKNLVVRMDGDDSKLVVSDDEI 485

Qy 489 -VWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWK----QDMERGNP 543
 :: | :| :|| :||:|||| | : :|: :: | |:: |

Db 486 LAIKLHRCGSDKITNCRECVSLQDPYCAWDNVELKCTAVGSPDWSAGKRRFIQNISLGEH 545

Qy 544 EWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPEASS 603
 : || |||: |::| | || :

Db 546 K-ACGG-----RPQT-----EIVASP-----VPTQPT 566

Qy 604 TVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPEL-----AGIPR 658
 | :| | | :| :||: ||:

Db 567 TKSSG-----DPVHSIHQA-----EFEPEIDNEIVIGVDD 596

Qy 659 EHVKVPLTRVS---GGAALAAQQSYWPHFVTVTVLFAVLVS--GALII-LVASPLRALRA 712
 :| :| | | :| :| | : | :| | ||:: :: | : |

Db 597 SNV-IPNTLAEINHAGSKLPSSQEKLPITYTAETLTIAIVTSCLGALVVGFI SGFLFSRRC 655

Qy 713 RGK 715
 ||:

Db 656 RGE 658

RESULT 14

T27165

hypothetical protein Y54E5B.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T27165

R;Lennard, N.

submitted to the EMBL Data Library, October 1998

A;Reference number: Z20321

A;Accession: T27165

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-712 <WIL>

A;Cross-references: EMBL:AL032653; PIDN:CAA21714.1; GSPDB:GN00019; CESP:Y54E5B.1

A;Experimental source: clone Y54E5B

C;Genetics:

A;Gene: CESP:Y54E5B.1

A;Map position: 1

A;Introns: 36/1; 70/2; 85/3; 194/2; 221/1; 253/3; 301/1; 352/3; 522/2; 560/1; 599/3; 655/3

Query Match 15.4%; Score 621.5; DB 2; Length 712;

Best Local Similarity 31.1%; Pred. No. 6.2e-41;

Matches 196; Conservative 97; Mismatches 233; Indels 105; Gaps 29;

Qy 68 LLSGDGNTLYVGAREAILALDIQDPGVPR LKNMIPWPASDRKKSECAFKKKSNETQCFNF 127
 ||: ||::| |||| | : | : | : | | || | || :| | |:

Db 57 LLAADGDSL LVGARNVYNLSLSTLSV---NHKIDWKPPAEHIEECIMKGKS-KTDCQNY 112

Qy 128 IRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP AHKHTAV 187
 |||| : ||| |||| | : : | : :|:| ||:| | :|:

Db 113 IRVLARKSAGVSLVCGTHAFSPKCREYTVTE---FGIRNTRQFDGQGIGISPYDPKHNSAL 169

Qy 188 LVDG--MLYSGTMNNFLGSEPILMR-TLGSQPVLKTDNFLRWLHHDA-----SFVAAIP 238

```

      | | | : | : : | : : : | | : | | : : | : | : | |
Db      170 YVPGTNQLFVATVTDFVGNDA LIYRK TIDETPSSKSAANI RTQSYDARVLNAPNFVATFA 229
Qy      239 STQVVYFFFEETASE-FDFFERLHT-SRVARVCKNDVGG EKLLQKKWTTFLKAQLLCTQP 296
      : | | : | | | | | | : | | | | | | | | : : | | : | | : |
Db      230 YKEHVYFWFREIASEAIDNNEEPQIYARVARVCKNDKGGARPANERWTSYLKARLNC SLP 289
Qy      297 -GQLP--FNVIRHAVLLPADSPTAPH-IYAVFTSQWQVGGTRSSAVCAFSLLDIERVF-K 351
      | | | : | | | : | | : | | : | | | | | : | | |
Db      290 SGSSPFYFNE LK-AVSDPIDAGNNNHVVYTVFST--PDS DVRMSAVCKFSMKKIREEF DN 346
Qy      352 GKYKELNKETSRWTTY-RGPETNPRPGSCSVGPSSDK---ALT FMKDHF LMD EQV--VG 404
      | : | | | : | | | | | | | | | : | : | | : |
Db      347 GTFKHQNNAQSMWMAFN RNEVPKPRPGSCS--PDSTKLPENTVSFILHHP L LHRPIPSVA 404
Qy      405 TPLLVKSG--VEYTRLAV-ETAQGLDGHS H LVMYLGTTTGS LHKAVVSGDSSAHLVEEIQ 461
      | | | : : | : : | : : | : : | : | | | : | : :
Db      405 APLLVEGADRADLTQITVLP R VRAVG GHNYDILFIGTSDGKVLK-VVEVDGNATVIQSAT 463
Qy      462 LFPDPEPVRNLQLAPTQGA VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWD PESR 521
      : | | : | | : : : : : : | | : | | : | | | |
Db      464 VFQRGVPIVN--LLTTKESV VIVSADEIASLPVHNCAQQTSCSKCVQLQDPHCAWDSSIA 521
Qy      522 TCCLLSAPNLNSWK-----QDMERGNPEWACASG-----PMSRSLRPQ 559
      | : | | | : | | | | | | | | : | | | :
Db      522 RCV-----HGGSWTGDQFIQNMVFGQSE-QCPEGIIVREV FDDNESEAQPEAVSRSGYPK 575
Qy      560 SRPQIIKEVLAVPNSILELPC-----PHLSALA---SYYWSHGPA A--- 597
      | : | | : | | | | | | | | | | : | | | |
Db      576 EHSTITVVLVA AVASLISLIIGAFIGIRVNRWAATSEPHRSASSTSGSDYDSFGRARLTR 635
Qy      598 -----VPEASSTVYNGS LLLIV 614
      | | : : | | : : :
Db      636 HDSLTTATKVDHGFVPQSKQSVDATSLVMSI 666

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RESULT 15

A49423

semaphorin I precursor - beetle (*Tribolium confusum*)

C;Species: *Tribolium confusum*

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999

C;Accession: A49423

R;Kolodkin, A.L.; Matthes, D.J.; Goodman, C.S.

Cell 75, 1389-1399, 1993

A;Title: The Semaphorin genes encode a family of transmembrane and secreted growth cone guidance molecules.

A;Reference number: A49423; MUID:94094332; PMID:8269517

A;Accession: A49423

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-711 <KOL>

A;Cross-references: GB:L26080

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Query Match          15.1%;  Score 609.5;  DB 2;  Length 711;
Best Local Similarity 31.4%;  Pred. No. 5.5e-40;
Matches 169;  Conservative 103;  Mismatches 214;  Indels 53;  Gaps 22;

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Qy 67 LLLSGDGNTLYVGAREAILALDIQDPGVPRLNMI PWPASDRKKSECAFKKKSNETQCFN 126
 Db 50 IVLNQDETSILVGGNRVYNLSIFDLS-ERKGGRIDWPSSDAHGQLCILKGKTDD-DCQN 107

Qy 127 FIRVLVSYNVTHLYTCGTFAFSPAC-TFIELQDSYLLPISEDKVMGKGQSPFDPAHKHT 185
 Db 108 YIRILYSSEPGLVICGTNSYKPLCRTYAFKEGKYL- ---EKEVEGIGLCPYNPEHNST 163

Qy 186 AVLVDGMLYSGTMNFFLGSEPILMRTLGSQPVLKTDFLRLHHDASFVAaipSTQVVYF 245
 Db 164 SVSYNGQLFSATVADFGGDPLIYR- ---EPQTELSDLKQL-NAPNFVNSVAYGDYIFF 218

Qy 246 FFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPF- --- 301
 Db 219 FYRETAVEYMNCCKVIYSRVARVCKDDKGGPHQSRDRWTSFLKARLNCsIPGEYPFYFDE 278

Qy 302 - - - - -NVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKE 356
 Db 279 IQSTSDIVEGRY- ---NSDDSKIYIGILTT- -PVNAIGGSAICAYQMA DILRVFEFSFKH 332

Qy 357 LNKETSRWTTYRGPET- - -NPRPGSCSVGPS- - -SDKALTFMKDHFMD- - -QVVGTPLL 408
 Db 333 QETINSNWLPV- -PQNLVPEPRPGQC-VRDSRILPDKNVNFikTHSLMEDVPALFGKPV 389

Qy 409 VKSGVEY- -TRLAVETAQGLDGHSHL-VMYLGTTTGS LHKAV- -VSGDSSAHLVEEIQ- - 461
 Db 390 VRVSLQYRFTAITVDPQVKTINNQYLDVLYIGTDDGKVLKAVNIPKRHAKALLYRKYRTS 449

Qy 462 LFPDPEPVRNLQLAPTQGAVFVGFGSGGVWRVPRANCSVYESCVDCVLARDPHCAWD PESR 521
 Db 450 VHPHGAPVKQLKIAPGYGKVVVGKDEIRLANLNHCASKTRCKDCVELQDPHCAWDAKQN 509

Qy 522 TCCLLSAPNLNSWK- - -QDMERGNPEWACASGPMsRLRPQSRPQIIKEVLAVPNSILE 577
 Db 510 LC- -VSIDTVTSYRFLIQDVVRGDDN-KCWSPQTDKKTVIKNKPSEVEN- -EITNSIDE 563

Search completed: May 5, 2004, 17:29:44
 Job time : 23 secs

OM protein - protein search, using sw model

Run on: May 5, 2004, 17:28:47 ; Search time 48 Seconds
(without alignments)
4394.610 Million cell updates/sec

Title: US-10-015-391A-277
Perfect score: 4031
Sequence: 1 MALPALGLDPWSLLGLFLFQ.....CRTSASDVDADNNCLGTEVA 761

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	DB	ID	Description
No.						

1	4031	100.0	761	10	US-09-759-130B-389	Sequence 389, App
2	4031	100.0	761	10	US-09-946-374-277	Sequence 277, App
3	4031	100.0	761	12	US-10-401-053A-2	Sequence 2, Appli
4	4031	100.0	761	12	US-10-006-485A-277	Sequence 277, App
5	4031	100.0	761	12	US-10-013-907A-277	Sequence 277, App
6	4031	100.0	761	12	US-10-015-499A-277	Sequence 277, App
7	4031	100.0	761	12	US-10-013-910A-277	Sequence 277, App
8	4031	100.0	761	12	US-10-226-254A-277	Sequence 277, App
9	4031	100.0	761	12	US-10-015-395A-277	Sequence 277, App
10	4031	100.0	761	13	US-10-042-431-19	Sequence 19, Appl
11	4031	100.0	761	14	US-10-006-856A-277	Sequence 277, App
12	4031	100.0	761	14	US-10-006-818A-277	Sequence 277, App
13	4031	100.0	761	14	US-10-015-393A-277	Sequence 277, App
14	4031	100.0	761	14	US-10-015-869A-277	Sequence 277, App
15	4031	100.0	761	14	US-10-012-121A-277	Sequence 277, App
16	4031	100.0	761	14	US-10-006-116A-277	Sequence 277, App
17	4031	100.0	761	14	US-10-006-117A-277	Sequence 277, App
18	4031	100.0	761	14	US-10-017-527A-277	Sequence 277, App
19	4031	100.0	761	14	US-10-013-913A-277	Sequence 277, App
20	4031	100.0	761	14	US-10-007-194A-277	Sequence 277, App
21	4031	100.0	761	14	US-10-013-430A-277	Sequence 277, App
22	4031	100.0	761	14	US-10-011-671A-277	Sequence 277, App
23	4031	100.0	761	14	US-10-012-755A-277	Sequence 277, App
24	4031	100.0	761	14	US-10-015-386A-277	Sequence 277, App
25	4031	100.0	761	14	US-10-011-692A-277	Sequence 277, App
26	4031	100.0	761	14	US-10-006-768A-277	Sequence 277, App
27	4031	100.0	761	14	US-10-017-610A-277	Sequence 277, App
28	4031	100.0	761	14	US-10-006-063A-277	Sequence 277, App
29	4031	100.0	761	14	US-10-020-063A-277	Sequence 277, App
30	4031	100.0	761	14	US-10-015-391A-277	Sequence 277, App
31	4031	100.0	761	14	US-10-017-407A-277	Sequence 277, App
32	4031	100.0	761	14	US-10-011-833A-277	Sequence 277, App
33	4031	100.0	761	14	US-10-006-041A-277	Sequence 277, App
34	4031	100.0	761	14	US-10-015-822A-277	Sequence 277, App
35	4031	100.0	761	14	US-10-015-387A-277	Sequence 277, App
36	4031	100.0	761	14	US-10-006-130A-277	Sequence 277, App
37	4031	100.0	761	14	US-10-006-172A-277	Sequence 277, App
38	4031	100.0	761	14	US-10-017-253A-277	Sequence 277, App
39	4031	100.0	761	14	US-10-015-392A-277	Sequence 277, App
40	4031	100.0	761	14	US-10-017-306A-277	Sequence 277, App
41	4031	100.0	761	14	US-10-017-867A-277	Sequence 277, App
42	4031	100.0	761	14	US-10-012-064A-277	Sequence 277, App
43	4031	100.0	761	14	US-10-013-909A-277	Sequence 277, App
44	4031	100.0	761	14	US-10-015-671A-277	Sequence 277, App
45	4031	100.0	761	14	US-10-015-610A-277	Sequence 277, App

ALIGNMENTS

RESULT 1
 US-09-759-130B-389
 ; Sequence 389, Application US/09759130B
 ; Publication No. US20030022279A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.

```

; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND
OTHER
; TITLE OF INVENTION: USES.
; FILE REFERENCE: MPI00-5350MNIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 761
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-389

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Query Match          100.0%; Score 4031; DB 10; Length 761;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60
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Db      1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60

Qy      61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKS 120
          |||
Db      61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKS 120

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Qy	121	ETQCFNFIRVLVSYNVTHLYTCGTFASFPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Db	121	ETQCFNFIRVLVSYNVTHLYTCGTFASFPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Qy	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST	240
Db	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST	240
Qy	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Db	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Qy	301	FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Db	301	FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Qy	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMLDEQVVGTPLLVKSGVEYTRLAV	420
Db	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMLDEQVVGTPLLVKSGVEYTRLAV	420
Qy	421	ETAQGLDGHSHLVMYLGTGSLHKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQGA	480
Db	421	ETAQGLDGHSHLVMYLGTGSLHKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQGA	480
Qy	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Db	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Qy	541	GNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Db	541	GNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Qy	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Db	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Qy	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE	720
Db	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE	720
Qy	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761
Db	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761

RESULT 2

US-09-946-374-277

; Sequence 277, Application US/09946374

; Publication No. US20030073129A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PlC1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
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; PRIOR APPLICATION NUMBER: 60/100385
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; PRIOR APPLICATION NUMBER: 60/100930
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; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
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; PRIOR APPLICATION NUMBER: 60/101071
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; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23

; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
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; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
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Query Match          100.0%; Score 4031; DB 10; Length 761;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60
      |||
Db      1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60

Qy     61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKSN 120
      |||
Db     61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKSN 120

Qy    121 ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP 180
      |||
Db    121 ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP 180

Qy    181 AHKHTAVLVDGMLYSGTMNIFLGSEPIILMRTLGSQPVLKTDNFLRWLHHDASFVAAPST 240
      |||
Db    181 AHKHTAVLVDGMLYSGTMNIFLGSEPIILMRTLGSQPVLKTDNFLRWLHHDASFVAAPST 240

Qy    241 QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP 300
      |||
Db    241 QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP 300

Qy    301 FNVIRHAVLLPADSPTAPIHYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE 360
      |||
Db    301 FNVIRHAVLLPADSPTAPIHYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE 360

Qy    361 TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV 420
      |||
Db    361 TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV 420

Qy    421 ETAQGLDGHSHLVMYLGTTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA 480
      |||
Db    421 ETAQGLDGHSHLVMYLGTTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA 480
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Qy	1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAYGDERRALSFFHQKG	60
Db	1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAYGDERRALSFFHQKG	60
Qy	61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGV PRLKNMIPWPASDRKKSECAFKKKSN	120
Db	61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGV PRLKNMIPWPASDRKKSECAFKKKSN	120
Qy	121 ETQCENFIRVLVSYNVTHLYTCGTFAFS PACTFIELQDSYLLPISEDKVMEGKGQSPFD	180

Db	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP	180
Qy	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST	240
Db	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST	240
Qy	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Db	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Qy	301	FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Db	301	FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Qy	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV	420
Db	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV	420
Qy	421	ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Db	421	ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Qy	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Db	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Qy	541	GNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Db	541	GNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Qy	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Db	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Qy	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE	720
Db	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE	720
Qy	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761
Db	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761

RESULT 4

US-10-006-485A-277

; Sequence 277, Application US/10006485A

; Publication No. US20030064062A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C9
; CURRENT APPLICATION NUMBER: US/10/006,485A
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
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; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60
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Db      1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60

Qy     61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSN 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSN 120

Qy    121 ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP 180

Qy    181 AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAI PST 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAI PST 240

Qy    241 QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP 300

Qy    301 FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE 360

Qy    361 TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV 420

Qy    421 ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA 480

Qy    481 VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLSWKQDMER 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLSWKQDMER 540
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Qy      541 GNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPE 600
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Db      541 GNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPE 600

Qy      601 ASSTVYNGSLLLLIVQDGVGGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 ASSTVYNGSLLLLIVQDGVGGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH 660

Qy      661 VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE 720

Qy      721 TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA 761
        ||||||||||||||||||||||||||||||||||||||||||||
Db      721 TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA 761

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RESULT 5

US-10-013-907A-277

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; Sequence 277, Application US/10013907A
; Publication No. US20030064925A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PlC34
; CURRENT APPLICATION NUMBER: US/10/013,907A
; CURRENT FILING DATE: 2001-12-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 277
; LENGTH: 761
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-907A-277

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Query Match          100.0%; Score 4031; DB 12; Length 761;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MALPALGLDPWSLLGLFLFQLLQLLLPPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60
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Db      1 MALPALGLDPWSLLGLFLFQLLQLLLPPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60

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Qy	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPR LKNMIPWPASDRKKSECAFKKSN	120
Db	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPR LKNMIPWPASDRKKSECAFKKSN	120
Qy	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP	180
Db	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP	180
Qy	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAPST	240
Db	181	AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAPST	240
Qy	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Db	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Qy	301	FN VIRHAVLLPADSPTAPIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Db	301	FN VIRHAVLLPADSPTAPIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Qy	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKS GVEYTRLAV	420
Db	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKS GVEYTRLAV	420
Qy	421	ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Db	421	ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Qy	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPE SRTCCLLSAPNLNSWKQDMER	540
Db	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPE SRTCCLLSAPNLNSWKQDMER	540
Qy	541	GNPEWACASGPM SRSRLPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Db	541	GNPEWACASGPM SRSRLPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Qy	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Db	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Qy	661	VKVPLTRVSGGAALAAQ QSYWPHFVTVTVLFAVL SGALIIIVASPLRALRARGKVQGCE	720
Db	661	VKVPLTRVSGGAALAAQ QSYWPHFVTVTVLFAVL SGALIIIVASPLRALRARGKVQGCE	720
Qy	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761
Db	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761

RESULT 6

US-10-015-499A-277

; Sequence 277, Application US/10015499A

; Publication No. US20030065142A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

```

; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C42
; CURRENT APPLICATION NUMBER: US/10/015,499A
; CURRENT FILING DATE: 2001-12-11
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 277
; LENGTH: 761
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-499A-277

```

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Query Match          100.0%; Score 4031; DB 12; Length 761;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60

Qy     61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSN 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSN 120

Qy    121 ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP 180

Qy    181 AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST 240

Qy    241 QVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 QVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP 300

Qy    301 FNVIRHAVLLPADSPTAPIHYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 FNVIRHAVLLPADSPTAPIHYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE 360

Qy    361 TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFILMDEQVVGTPLLVKSGVEYTRLAV 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFILMDEQVVGTPLLVKSGVEYTRLAV 420

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Qy	421	ETAQGLDGHSHLVMYLGT'TTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Db	421	ETAQGLDGHSHLVMYLGT'TTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Qy	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPE SRTCCLLSAPNLNSWKQDMER	540
Db	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPE SRTCCLLSAPNLNSWKQDMER	540
Qy	541	GNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSI LELPCPHLSALASYWSHGPAAVPE	600
Db	541	GNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSI LELPCPHLSALASYWSHGPAAVPE	600
Qy	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Db	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Qy	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIIILVASPLRALRARGKVQGCE	720
Db	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIIILVASPLRALRARGKVQGCE	720
Qy	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761
Db	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761

RESULT 7

US-10-013-910A-277

; Sequence 277, Application US/10013910A

; Publication No. US20030187192A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C33

; CURRENT APPLICATION NUMBER: US/10/013,910A

; CURRENT FILING DATE: 2001-12-10

; PRIOR APPLICATION NUMBER: 60/098716

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098723

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098749

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098750

; PRIOR FILING DATE: 1998-09-01

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; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 277
; LENGTH: 761
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-910A-277

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Query Match          100.0%; Score 4031; DB 12; Length 761;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy      1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60

Qy     61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSN 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSN 120

Qy    121 ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP 180

Qy    181 AHKHTAVLVDGMLYSGTMNIFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAaipST 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AHKHTAVLVDGMLYSGTMNIFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAaipST 240

Qy    241 QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP 300

Qy    301 FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE 360

Qy    361 TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAV 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAV 420

Qy    421 ETAQGLDGHSHLVMYLGTTTGSLHKAVVSGDSSAHLVEEIQLEFPDPEPVRNLQLAPTQGA 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ETAQGLDGHSHLVMYLGTTTGSLHKAVVSGDSSAHLVEEIQLEFPDPEPVRNLQLAPTQGA 480

Qy    481 VFVGFSGGVWRVPRANCsvYESCVDCVLARDPHCAWDPEsRTCCLLSAPNLNSWKQDMER 540

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Db	481	V F V G F S G G V W R V P R A N C S V Y E S C V D C V L A R D P H C A W D P E S R T C C L L S A P N L N S W K Q D M E R	540
Qy	541	G N P E W A C A S G P M S R S L R P Q S R P Q I I K E V L A V P N S I E L P C P H L S A L A S Y Y W S H G P A A V P E	600
Db	541	G N P E W A C A S G P M S R S L R P Q S R P Q I I K E V L A V P N S I E L P C P H L S A L A S Y Y W S H G P A A V P E	600
Qy	601	A S S T V Y N G S L L L I V Q D G V G G L Y Q C W A T E N G F S Y P V I S Y W V D S Q D Q T L A L D P E L A G I P R E H	660
Db	601	A S S T V Y N G S L L L I V Q D G V G G L Y Q C W A T E N G F S Y P V I S Y W V D S Q D Q T L A L D P E L A G I P R E H	660
Qy	661	V K V P L T R V S G G A A L A A Q Q S Y W P H F V T V T V L F A L V L S G A L I I L V A S P L R A L R A R G K V Q G C E	720
Db	661	V K V P L T R V S G G A A L A A Q Q S Y W P H F V T V T V L F A L V L S G A L I I L V A S P L R A L R A R G K V Q G C E	720
Qy	721	T L R P G E K A P L S R E Q H L Q S P K E C R T S A S D V D A D N N C L G T E V A	761
Db	721	T L R P G E K A P L S R E Q H L Q S P K E C R T S A S D V D A D N N C L G T E V A	761

RESULT 8

US-10-226-254A-277

; Sequence 277, Application US/10226254A

; Publication No. US20030224478A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C68

; CURRENT APPLICATION NUMBER: US/10/226,254A

; CURRENT FILING DATE: 2002-08-21

; PRIOR APPLICATION NUMBER: 60/098716

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098723

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098749

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098750

; PRIOR FILING DATE: 1998-09-01

; PRIOR APPLICATION NUMBER: 60/098803

; PRIOR FILING DATE: 1998-09-02

; PRIOR APPLICATION NUMBER: 60/098821

; PRIOR FILING DATE: 1998-09-02

; PRIOR APPLICATION NUMBER: 60/098843

```
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 277
;   LENGTH: 761
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-226-254A-277
```

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Query Match          100.0%;   Score 4031;   DB 12;   Length 761;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches 761;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;
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Qy      1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60
      |||
Db      1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60

Qy     61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKS 120
      |||
Db     61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKS 120

Qy    121 ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGEGKGQSPFDP 180
      |||
Db    121 ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGEGKGQSPFDP 180

Qy    181 AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLTNDNFRWLHHDASFVAaipst 240
      |||
Db    181 AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLTNDNFRWLHHDASFVAaipst 240

Qy    241 QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP 300
      |||
Db    241 QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP 300

Qy    301 FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE 360
      |||
Db    301 FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE 360

Qy    361 TSRWTTYRGPETNPRPGSCSVGPSSDKALTfMKDHFLMDEQVVGTPLLVKSGVEYTRLAV 420
      |||
Db    361 TSRWTTYRGPETNPRPGSCSVGPSSDKALTfMKDHFLMDEQVVGTPLLVKSGVEYTRLAV 420

Qy    421 ETAQGLDGHSHLVMYLGTtTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA 480
      |||
Db    421 ETAQGLDGHSHLVMYLGTtTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA 480

Qy    481 VFVGfSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPEsRTCCLLSAPNLNSWKQDMER 540
      |||
Db    481 VFVGfSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPEsRTCCLLSAPNLNSWKQDMER 540

Qy    541 GNPEWACASGPMsRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE 600
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Db	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPR LKNMIPWPASDRKKSECAFKKKS	120
Qy	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Db	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Qy	181	AHKHTAVLVDGMLYSGTMN N FLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST	240
Db	181	AHKHTAVLVDGMLYSGTMN N FLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST	240
Qy	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQILLCTQPGQLP	300
Db	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQILLCTQPGQLP	300
Qy	301	FNVIRHAVLLPADSPTAPIHYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Db	301	FNVIRHAVLLPADSPTAPIHYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Qy	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV	420
Db	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV	420
Qy	421	ETAQGLDGHSHLVMYLGT T T T GSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Db	421	ETAQGLDGHSHLVMYLGT T T T GSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Qy	481	VFVGFGG VWRVPRANC SVYESCVDCLARDPHCAWDPE SRTCCLLSAPNLNSWKQDMER	540
Db	481	VFVGFGG VWRVPRANC SVYESCVDCLARDPHCAWDPE SRTCCLLSAPNLNSWKQDMER	540
Qy	541	GNPEWACASGPM SRSR L P QSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Db	541	GNPEWACASGPM SRSR L P QSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Qy	601	ASSTVYNGS L L L I V Q D G V G G L Y Q C W A T E N G F S Y P V I S Y W V D S Q D Q T L A L D P E L A G I P R E H	660
Db	601	ASSTVYNGS L L L I V Q D G V G G L Y Q C W A T E N G F S Y P V I S Y W V D S Q D Q T L A L D P E L A G I P R E H	660
Qy	661	VKVPLTRVSGGAALAAQ QSYWPHFVTVTVL FALVLSGALIIIVASPLRALRARGKVQGCE	720
Db	661	VKVPLTRVSGGAALAAQ QSYWPHFVTVTVL FALVLSGALIIIVASPLRALRARGKVQGCE	720
Qy	721	TLRPGEKAPLSREQHLQSPKECRTSASD V D A D N N C L G T E V A	761
Db	721	TLRPGEKAPLSREQHLQSPKECRTSASD V D A D N N C L G T E V A	761

RESULT 10

US-10-042-431-19

; Sequence 19, Application US/10042431

; Publication No. US20020182675A1

; GENERAL INFORMATION:

; APPLICANT: MCCARTHY, Sean A

; APPLICANT: BARNES, Thomas M

; APPLICANT: FRASER, Christopher C

; APPLICANT: SHARP, John D

; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,

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; TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
; FILE REFERENCE: 10147-6U2
; CURRENT APPLICATION NUMBER: US/10/042,431
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 761
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-431-19
```

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Query Match          100.0%; Score 4031; DB 13; Length 761;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60

Qy     61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKSN 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKSN 120

Qy    121 ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP 180

Qy    181 AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAaipst 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAaipst 240

Qy    241 QVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 QVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP 300

Qy    301 FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE 360

Qy    361 TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV 420

Qy    421 ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA 480

Qy    481 VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPEsrtCCLLSAPNLNSWKQDMER 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPEsrtCCLLSAPNLNSWKQDMER 540

Qy    541 GNPEWACASGPMsRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE 600
```

```

Db      541  |||||GNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE 600
Qy      601  ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH 660
Db      601  |||||ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH 660
Qy      661  VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIIILVASPLRALRARGKVQGCE 720
Db      661  |||||VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIIILVASPLRALRARGKVQGCE 720
Qy      721  TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA 761
Db      721  |||||TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA 761

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RESULT 11

US-10-006-856A-277

; Sequence 277, Application US/10006856A

; Publication No. US20030044841A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C14

; CURRENT APPLICATION NUMBER: US/10/006,856A

; CURRENT FILING DATE: 2002-05-10

; NUMBER OF SEQ ID NOS: 477

; Prior Application removed - See File Wrapper or Palm

; SEQ ID NO 277

; LENGTH: 761

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-006-856A-277

Query Match 100.0%; Score 4031; DB 14; Length 761;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1  MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60
Db      1  |||||MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60
Qy      61  LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKS 120

```

Db	61		LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKS	120
Qy	121		ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Db	121		ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Qy	181		AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDAFVAaipst	240
Db	181		AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDAFVAaipst	240
Qy	241		QVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Db	241		QVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Qy	301		FNvirHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Db	301		FNvirHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Qy	361		TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFILMDEQVVGTPLLVKSGVEYTRLAV	420
Db	361		TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFILMDEQVVGTPLLVKSGVEYTRLAV	420
Qy	421		ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Db	421		ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Qy	481		VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPEsRTCCLLSAPNLNSWKQDMER	540
Db	481		VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPEsRTCCLLSAPNLNSWKQDMER	540
Qy	541		GNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Db	541		GNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Qy	601		ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Db	601		ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Qy	661		VKVPLTRVSGGAALAAQSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE	720
Db	661		VKVPLTRVSGGAALAAQSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE	720
Qy	721		TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761
Db	721		TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761

RESULT 12

US-10-006-818A-277

; Sequence 277, Application US/10006818A

; Publication No. US20030054406A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

```

; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C4
; CURRENT APPLICATION NUMBER: US/10/006,818A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 277
; LENGTH: 761
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-006-818A-277

```

```

Query Match          100.0%; Score 4031; DB 14; Length 761;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy      1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60
      |||
Db      1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60

Qy     61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMI PWPASDRKKSECAFKKSN 120
      |||
Db     61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMI PWPASDRKKSECAFKKSN 120

Qy    121 ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP 180
      |||
Db    121 ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP 180

Qy    181 AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAPST 240
      |||
Db    181 AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAPST 240

Qy    241 QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP 300
      |||
Db    241 QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP 300

Qy    301 FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE 360
      |||
Db    301 FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE 360

Qy    361 TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV 420
      |||
Db    361 TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV 420

Qy    421 ETAQGLDGHSHLVMYLGTTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA 480
      |||

```



```

Db      421 ETAQGLDGHSHLVMYLGT'TTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA 480
Qy      481 VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPE SRTCCLLSAPNLNSWKQDMER 540
        |||||||||||||||||||||||||||||||||||||||||||
Db      481 VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPE SRTCCLLSAPNLNSWKQDMER 540
Qy      541 GNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYW SHGPAAVPE 600
        |||||||||||||||||||||||||||||||||||||||||||
Db      541 GNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYW SHGPAAVPE 600
Qy      601 ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH 660
        |||||||||||||||||||||||||||||||||||||||||||
Db      601 ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH 660
Qy      661 VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFAVLVSGALIIIVASPLRALRARGKVQGCE 720
        |||||||||||||||||||||||||||||||||||||||||||
Db      661 VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFAVLVSGALIIIVASPLRALRARGKVQGCE 720
Qy      721 TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA 761
        |||||||||||||||||||||||||||||||||||||||||||
Db      721 TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA 761

```

RESULT 13

US-10-015-393A-277

; Sequence 277, Application US/10015393A

; Publication No. US20030069179A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C46

; CURRENT APPLICATION NUMBER: US/10/015,393A

; CURRENT FILING DATE: 2002-06-10

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 277

; LENGTH: 761

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-015-393A-277

```

Query Match          100.0%;  Score 4031;  DB 14;  Length 761;
Best Local Similarity 100.0%;  Pred. No. 0;

```

	Matches	761;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1		MALPALGLDPWSLLGLFLFQLLQLLLP	TTTTAGGGGQGPM	PRVRYAGDERRALSFFHQKG	60				
Db	1		MALPALGLDPWSLLGLFLFQLLQLLLP	TTTTAGGGGQGPM	PRVRYAGDERRALSFFHQKG	60				
Qy	61		LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGV	PRLKNMIPWPASDRKKSECAFKKSN	120					
Db	61		LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGV	PRLKNMIPWPASDRKKSECAFKKSN	120					
Qy	121		ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTF	IELQDSYLLPISEDKVM	EGKGQSPFDP	180				
Db	121		ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTF	IELQDSYLLPISEDKVM	EGKGQSPFDP	180				
Qy	181		AHKHTAVLVDGMLYSGTMN	FLGSEPILMRTLGSQPVLKTDN	FLRWLHHDAFVA	AI	PST	240		
Db	181		AHKHTAVLVDGMLYSGTMN	FLGSEPILMRTLGSQPVLKTDN	FLRWLHHDAFVA	AI	PST	240		
Qy	241		QVYFFFEETASEFDFFERLH	TSRVARVCKNDVGGEKLLQKKW	TTF	LKAQLLCTQPGQLP	300			
Db	241		QVYFFFEETASEFDFFERLH	TSRVARVCKNDVGGEKLLQKKW	TTF	LKAQLLCTQPGQLP	300			
Qy	301		FNVI	RHAVLLPADSPTAPHIYAVFTS	QWQVGGTRSSAVCAFSL	LDIERVFKGKYKELNKE	360			
Db	301		FNVI	RHAVLLPADSPTAPHIYAVFTS	QWQVGGTRSSAVCAFSL	LDIERVFKGKYKELNKE	360			
Qy	361		TSRW	TTYRGPETNPRPGSCSVGPSSDKALT	FMKDHFLMDEQVVG	TPLLVKSGVEYTRLAV	420			
Db	361		TSRW	TTYRGPETNPRPGSCSVGPSSDKALT	FMKDHFLMDEQVVG	TPLLVKSGVEYTRLAV	420			
Qy	421		ETAQGLDGHSHLVMYL	GTTTGS	LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQ	LAPTQGA	480			
Db	421		ETAQGLDGHSHLVMYL	GTTTGS	LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQ	LAPTQGA	480			
Qy	481		VFVG	FSGGVWRVPRANCSVYES	CVDCVLARDPHCAWD	PESRTCCLLSAPNLSWKQD	MER	540		
Db	481		VFVG	FSGGVWRVPRANCSVYES	CVDCVLARDPHCAWD	PESRTCCLLSAPNLSWKQD	MER	540		
Qy	541		GNPEWACASGPMSRSLRPQSRPQI	IKEVLAVPNSILELPCPHLSALASYYWSHG	PAAVPE	600				
Db	541		GNPEWACASGPMSRSLRPQSRPQI	IKEVLAVPNSILELPCPHLSALASYYWSHG	PAAVPE	600				
Qy	601		ASSTVYNGSLLLIVQDGVGG	LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGI	PREH	660				
Db	601		ASSTVYNGSLLLIVQDGVGG	LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGI	PREH	660				
Qy	661		VKVPLTRVSGGAALAAQ	QSYWPHFVTVTVLFALVLSGALII	LVASPLRALRARGKVQ	GCE	720			
Db	661		VKVPLTRVSGGAALAAQ	QSYWPHFVTVTVLFALVLSGALII	LVASPLRALRARGKVQ	GCE	720			
Qy	721		TLRPG	EKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761					
Db	721		TLRPG	EKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761					

RESULT 14
US-10-015-869A-277

```

; Sequence 277, Application US/10015869A
; Publication No. US20030073130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C45
; CURRENT APPLICATION NUMBER: US/10/015,869A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 277
; LENGTH: 761
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-869A-277

```

```

Query Match          100.0%; Score 4031; DB 14; Length 761;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG 60

Qy     61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSN 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSN 120

Qy    121 ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP 180

Qy    181 AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPST 240

Qy    241 QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP 300

Qy    301 FNVIRHAVLLPADSPTAPIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 FNVIRHAVLLPADSPTAPIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE 360

```

Qy	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV	420
Db	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV	420
Qy	421	ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFDPDPEPVRNLQLAPTQGA	480
Db	421	ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFDPDPEPVRNLQLAPTQGA	480
Qy	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Db	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Qy	541	GNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Db	541	GNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Qy	601	ASSTVYNGSLLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Db	601	ASSTVYNGSLLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Qy	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE	720
Db	661	VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE	720
Qy	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761
Db	721	TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761

RESULT 15

US-10-012-121A-277

; Sequence 277, Application US/10012121A

; Publication No. US20030073810A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan l.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C20

; CURRENT APPLICATION NUMBER: US/10/012,121A

; CURRENT FILING DATE: 2001-12-07

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 277

; LENGTH: 761
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-121A-277

Query Match 100.0%; Score 4031; DB 14; Length 761;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG	60
Db	1	MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG	60
Qy	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSN	120
Db	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSN	120
Qy	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Db	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Qy	181	AHKHTAVLVDGMLYSGTMNIFLGSEPIILMRTLGSQPVLKTDNFLRWLHHDASFVAAPST	240
Db	181	AHKHTAVLVDGMLYSGTMNIFLGSEPIILMRTLGSQPVLKTDNFLRWLHHDASFVAAPST	240
Qy	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Db	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Qy	301	FNVIHVALLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Db	301	FNVIHVALLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Qy	361	TSRWT'TYRGPETNPRPGSCSVGPSSDKALT'FMKDHF'LMDEQVVGTP'LLVKS'GVEYTRLAV	420
Db	361	TSRWT'TYRGPETNPRPGSCSVGPSSDKALT'FMKDHF'LMDEQVVGTP'LLVKS'GVEYTRLAV	420
Qy	421	ETAQGLDGHSHLVMYLGTTT'GSLHK'AVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Db	421	ETAQGLDGHSHLVMYLGTTT'GSLHK'AVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Qy	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPE'SRTCCLLSAPNLSWKQDMER	540
Db	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPE'SRTCCLLSAPNLSWKQDMER	540
Qy	541	GNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Db	541	GNPEWACASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPE	600
Qy	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Db	601	ASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Qy	661	VKVPLTRVSGGAALAAQ'QSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE	720
Db	661	VKVPLTRVSGGAALAAQ'QSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCE	720

Qy 721 TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA 761
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 721 TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA 761

Search completed: May 5, 2004, 17:32:25
Job time : 51 secs

OM protein - protein search, using sw model

```
Run on:      May  5, 2004, 17:26:32 ; Search time 52 Seconds
              (without alignments)
              4617.488 Million cell updates/sec
```

```
Title:          US-10-015-391A-277
Perfect score:  4031
Sequence:       1 MALPALGLDPWSLLGLFLFQ.....CRTSASDVADANNCLGTEVA 761
```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				Description
No.	Score	Match	Length	DB	ID	
%						

1	1743	43.2	328	4	Q9HA40	Q9ha40 homo sapien
2	1239.5	30.7	823	11	Q8BIR6	Q8bir6 mus musculu
3	1097	27.2	963	4	Q9C0C4	Q9c0c4 homo sapien
4	1067.5	26.5	550	11	Q8BIC3	Q8bic3 mus musculu
5	1041	25.8	862	4	Q7Z5S4	Q7z5s4 homo sapien
6	1034.5	25.7	681	4	Q7Z3N1	Q7z3n1 homo sapien
7	995	24.7	799	11	Q8BJC1	Q8bjc1 mus musculu
8	882	21.9	722	11	Q810B2	Q810b2 mus musculu
9	854.5	21.2	756	13	Q8QGU9	Q8qgu9 gallus gall
10	847	21.0	774	13	Q8JIW9	Q8jiw9 xenopus lae
11	817.5	20.3	748	4	Q8TB71	Q8tb71 homo sapien
12	788	19.5	777	11	Q8BMF6	Q8bmf6 mus musculu
13	787	19.5	777	11	Q8BH34	Q8bh34 mus musculu
14	737	18.3	782	4	Q9NS98	Q9ns98 homo sapien
15	736	18.3	635	4	Q96GX0	Q96gx0 homo sapien
16	709.5	17.6	775	11	Q9QX23	Q9qx23 mus musculu
17	709	17.6	645	4	Q7Z5X0	Q7z5x0 homo sapien
18	699	17.3	1122	11	Q7TT33	Q7tt33 mus musculu
19	688.5	17.1	844	11	Q8BXU8	Q8bxu8 mus musculu
20	678.5	16.8	587	11	Q8BUT0	Q8but0 mus musculu
21	678.5	16.8	605	11	Q8BXZ7	Q8bxz7 mus musculu
22	672.5	16.7	1073	4	Q8NFY4	Q8nfy4 homo sapien
23	668	16.6	687	4	Q9BXR8	Q9bxr8 homo sapien
24	652	16.2	1017	4	Q8NFY5	Q8nfy5 homo sapien
25	650	16.1	1022	4	Q9P249	Q9p249 homo sapien
26	649.5	16.1	998	4	Q8NFY6	Q8nfy6 homo sapien
27	649.5	16.1	1009	11	Q80TD0	Q80td0 mus musculu
28	643	16.0	1011	4	Q8NFY3	Q8nfy3 homo sapien
29	642.5	15.9	1005	11	Q9EQ71	Q9eq71 mus musculu
30	635	15.8	595	11	Q8BKG8	Q8bkg8 mus musculu
31	623.5	15.5	452	13	Q7T165	Q7t165 brachydanio
32	615.5	15.3	963	11	Q91Y36	Q91y36 mus musculu
33	602.5	14.9	697	5	Q8MLF1	Q8mlf1 drosophila
34	602.5	14.9	724	5	Q9V7Q7	Q9v7q7 drosophila
35	583	14.5	770	5	O44253	O44253 drosophila
36	581	14.4	770	5	Q9V3M4	Q9v3m4 drosophila
37	556	13.8	418	4	Q96JU9	Q96ju9 homo sapien
38	556	13.8	457	4	Q9HBR1	Q9hbr1 homo sapien
39	554	13.7	403	11	Q8BKQ6	Q8bkq6 mus musculu
40	551	13.7	616	5	Q9V7P8	Q9v7p8 drosophila
41	542	13.4	476	4	Q8NFY7	Q8nfy7 homo sapien
42	523.5	13.0	923	11	Q8R4U3	Q8r4u3 mus musculu
43	515.5	12.8	920	11	Q8R4U4	Q8r4u4 rattus norv
44	496.5	12.3	367	4	Q9HAH9	Q9hah9 homo sapien
45	494.5	12.3	1091	5	Q7YU67	Q7yu67 drosophila

ALIGNMENTS

RESULT 1

Q9HA40

ID	Q9HA40	PRELIMINARY;	PRT;	328 AA.
AC	Q9HA40;			
DT	01-MAR-2001	(TrEMBLrel. 16, Created)		
DT	01-MAR-2001	(TrEMBLrel. 16, Last sequence update)		
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)		


```

DE   Hypothetical protein FLJ12287.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Mammary gland;
RA   Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA   Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA   Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA   Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA   Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA   Ninomiya K., Iwayanagi T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK022349; BAB14018.1; -.
DR   GO; GO:0005622; C:intracellular; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003684; F:damaged DNA binding; IEA.
DR   GO; GO:0008094; F:DNA dependent ATPase activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0007275; P:development; IEA.
DR   GO; GO:0006310; P:DNA recombination; IEA.
DR   GO; GO:0006281; P:DNA repair; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000005; HTHAraC.
DR   InterPro; IPR003659; Plexin-like.
DR   InterPro; IPR002165; Plexin_repeat.
DR   InterPro; IPR001553; RecA.
DR   InterPro; IPR001627; Sema.
DR   Pfam; PF01437; PSI; 1.
DR   Pfam; PF01403; Sema; 1.
DR   PRINTS; PR00142; RECA.
DR   SMART; SM00423; PSI; 1.
DR   PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
KW   Hypothetical protein.
SQ   SEQUENCE 328 AA; 35403 MW; 6F455687BFCEB2312 CRC64;

```

QY 614 VQDGVGGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAA 673
 |||
 Db 181 VQDGVGGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAA 240
 QY 674 LAAQQSYWPHFVTVTVLFAVLVSGALIIILVASPLRALRARGKVQGCETLRPGKAPLSRE 733
 |||
 Db 241 LAAQQSYWPHFVTVTVLFAVLVSGALIIILVASPLRALRARGKVQGCETLRPGKAPLSRE 300
 QY 734 QHLQSPKECRTSASDVADANNCLGTEVA 761
 |||
 Db 301 QHLQSPKECRTSASDVADANNCLGTEVA 328

RESULT 2

Q8BIR6

ID Q8BIR6 PRELIMINARY; PRT; 823 AA.
 AC Q8BIR6;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Semaphorin 4B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Ovary, and Uterus;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK030331; BAC26906.1; -.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0007275; P:development; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000005; HTHAraC.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
 SQ SEQUENCE 823 AA; 91485 MW; E3B8C5E5CFA1CD45 CRC64;

Query Match 30.7%; Score 1239.5; DB 11; Length 823;
 Best Local Similarity 37.6%; Pred. No. 1.7e-97;
 Matches 295; Conservative 128; Mismatches 289; Indels 73; Gaps 24;

Qy 13 LLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQDFDTLLLSGD 72
 || | : || || || | ||: : | : : : |||| |
 Db 11 LLSLMVLLLLLLLLWTTTTRALG-----PRINVPLCCQERLIRKFEAENISNYTALLLSQD 65
 Qy 73 GNTLYVGAREAILALDIQDPGVP--RLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRV 130
 | ||||| ||| : ||: : | : : : | | : | : || | : | | : ||:
 Db 66 GKTLYVGAREALFALNSNLSFLPGGEYQELL-WSADADRKQQCSFKGKDPKRDCQNYIKI 124
 Qy 131 LVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVM--EGKGQSPFDPAHKHTAVL 188
 | : | : || |||| |||| | : | : | : ||| : |||| | ||||:
 Db 125 LLPLNSSHLLTCGTAAFSPLCAYIHIASTLAQDEAGNVILEDGKGRCPFDPNFKSTALV 184
 Qy 189 VDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAA-----IP 238
 ||| ||| : || : || : | : | || : | || | : ||| : |
 Db 185 VDGElyTGTVSSFQGNDAISRSQSSRPT-KTESSLNWL-QDPAFVASAYVPESLGSPIG 242
 Qy 239 STQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQ 298
 : |||| || ||: ||| ||||| || ||| : || : || : ||||| : ||:
 Db 243 DDDRIYFFFSETGQEFEFFENTIVSRVARVCKGDEGGERVLQQRWTSFLKAQLLCSRPD 302
 Qy 299 -LPFNVIRHAVLL---PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKY 354
 |||| : | | | | |||| | | ||: | : : | : | | |
 Db 303 GFPPFNLQDVFTLNPNPQDW-RKTLFYGVFTSQWHRGTTEGSAICVFTMNDVQKAFDGLY 361
 Qy 355 KELNKETSRTWTTYRGPETNPRPGSCSVGPS-----SDKALTFMKDHFLLMDEQVV 403
 | : : || : | | |||| : : | : | | : |||| | |
 Db 362 KKVNETQQWYTETHQVPTPRPGACITNSARERKINSSLQLPDRVLNFKDHFLLMDGQVR 421
 Qy 404 GTPLLVKSGVEYTRLAVETAQGLDGHS-HLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQL 462
 || : | | : || || || : | : || | |||| | | : : || : |
 Db 422 SRLLLLQPRARYQRVAVHRVPGL--HSTYDVLFLGTGDGR LHKAVTL-SSRVHIIIEELQI 478
 Qy 463 FPDPEPVRNLQLAPTQGA FVGFGSGGVWRVPRANCSVYESCVDCVLARDPHCAWD PESRT 522
 || : || : || | | : || : || |||| : | | || : |||| : || :
 Db 479 FPQGPVQNL LLD SHGGLLYASSHSGVVQVPVANC SLYP TCGDC LLARDPYCAWTGSACR 538
 Qy 523 CCLLSAPNLNS--WKQDMERGNPEWACASGPM SRS LRPQSRPQIIKEVLAVPNSILELPC 580
 | | : | | | || : : | : | | : | | || : | |
 Db 539 LASLYKPD LASRPWTQDIEGASVKELCKN SSYKARFLVPGKP--CKQVQIQPNTVNTLAC 596
 Qy 581 PHLSALASYW SHGPAAVPEASS--TVYNGS LLLI-VQDGVGGLYQCWATENGFSYPVIS 637
 | || || : | | | | : || : | ||| : | | : || : || : | | | |
 Db 597 PLLSNLATRLWVHNGAPVNASASCRVLPTGDL LLVGSQQGL-GVFQCWSIEEGFQQLVAS 655
 Qy 638 YWVDSQDQ-TLALDPELAGIPREHVKVPLTRVS----GGAALAAQ QSYWPHFVTVTVLFA 692
 | : : : : | | | : : || | | : | : || | : : ||
 Db 656 YCPEVMEEGVMDQKNQRD GTP---VIINTSRVSAPAGGRASWGADKSYWNEFLVMCTLFV 712
 Qy 693 LVLSGALIILVASPLRALRARGKVQCETLRPG EKAPLSREQHLQSPKECRTSASDV DAD 752
 : : | : : | | : | : : : | | |
 Db 713 FAMVLLFLFLLYRHRDGMKFLKQGE CASVHP-----KTRPIVLPPETRPL----- 758
 Qy 753 NNCLG 757
 ||:|
 Db 759 -NCVG 762

Q9C0C4

Query Match 27.2%; Score 1097; DB 4; Length 963;
Best Local Similarity 36.6%; Pred. No. 4e-85;
Matches 291; Conservative 101; Mismatches 288; Indels 116; Gaps 28;

Qy	6	LGLDPWSLLGLFLFQLLQL-----LLPTTTAGGGG-----QGMPRVRYAGD	48
Db	107	LGRPRWGCQGQRLFQKCPLLPIRGFGWHLLVAWGAGSRGARLRAVEPQGSCPSAAMLTPA	166
Qy	49	E-----RRALSFFHQKGLQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPW	103
Db	167	ELATVVRR---FSQTGIQDFLTTLTLEPTGLLYVGAREALFAFSME---ALELQGAISW	219
Qy	104	PASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLP	163
Db	220	EAPVEKKTECIQKGKNNQTECFNFIRFLQPYNASHLYVCGTYAFQPKCTYVNM---LTFT	276

QY 164 ISEDKVMGKQSPFDPAHKHTAVLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNF 223
 : : :|||: |:||| | :||| ||| |:||||:||||:| :| :||:
 Db 277 LEHGEFEDGKGKCPYDPAKGHAGLLVDGELYSATLNNFLGTEPIILRNMGPHHSMKTEYL 336

QY 224 LRWLHHDASFV--AAIPST-----QVVYFFFEETASEFDFFERLHTSRVARVCKNDV 273
 || :: || | :| : |||| | | | : :|||||| |:
 Db 337 AFWL-NEPHFVGSAIVPESVGSFTGDDDKVYFFFRERAVESDCYAEQVVARVARVCKGDM 395

QY 274 GGEKLLQKKWTTFLKAQLLCTQPG-QLPFNIRHAVLLPADSPTAPHIYAVFTSQWQVGG 332
 || : ||:|||||||:| |: | || || : | : || :|| |
 Db 396 GGARTLQRKWTTFLKARLACSAPNWQLYFNQLQAMHTLQDTSWHNTTFFGVFQAQW--GD 453

QY 333 TRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNPRPGSC-----SV 381
 ||:| : | :|||:| ||| ::| :| | | :||||| |
 Db 454 MYLSAICEYQLEEIQRVFEQPYKEYHEEAQKWDRTDPVPSRPGSCINNWHRRHGYTSS 513

QY 382 GPSSDKALTFMKDHFMDQV---VGTPLLVKSGVEYTRLAVETAQGLDGHSHLVMYLG 438
 | | |:| | ||:|||| |||| | :| | : |||| :: |::||
 Db 514 LELPDNINLNFVKKHPLMEEQVGRWSRPLLVKKGTNFTHLVADRVTLGDGATYTVLFIGT 573

QY 439 TTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGAFFVGFSGGVWRVPRANCS 498
 | | ||| | ||:|:| | ||:|:| |: :: :| | : ::| |:|
 Db 574 GDGWLLKAVSLG--PWVHLIEELQLF-DQEPMSIVLSQSKLLFAGSRSQVLPVADCM 631

QY 499 VYESCVDCVLARDPHCAWDPESTRCCLLSAPNLSWKQDMERGNPEWAC-ASGPMRSRLR 557
 | || |||||:|:| : | : : : | : : | | |: :|
 Db 632 KYRSCADCVLARDPYCAWSVNTSRCVAVGGHSGSLLIQHVMTSDTSGICNLRG--SKKVR 689

QY 558 PQSRPQIIKEVLAVPNSILELPCPHLSA-LASYWWSHGPAAVP--EASSTVYNGSLLLIV 614
 | : | : | || |||: || | : | : | : | :| :|
 Db 690 PTP-----KNITVVAGTDLVLPC-HLSSNLAHARWTFGGRDLPAEQPGSFYDARLQALV 743

QY 615 ----QDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSG 670
 | | | |:| | || : | : | | :
 Db 744 VMAAQPRHAGAYHCFSEEQG-----ARLAAEGYLVAV----VAGPSVTLEA 785

QY 671 GAALAAQQSYWPHFVTVTVLFAVLVSGALIILVASPLRALRARGKVQGCETLRPGEKA-- 728
 | | | : | | |: | |:| | | | | | | |
 Db 786 RAPLENLGLVW---LAVVALGAVCL--VLLLLVLSLRRRLR-----EELEKGAKATE 832

QY 729 -----PLSREQHLQSP 739
 || : ||
 Db 833 RTLVPLELPKEPTSP 848

RESULT 4

Q8BIC3

ID Q8BIC3 PRELIMINARY; PRT; 550 AA.
 AC Q8BIC3;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Semaphorin 4B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL; AK028896; BAC26181.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 SQ SEQUENCE 550 AA; 61309 MW; 8C28E29DC4CAC958 CRC64;

Query Match 26.5%; Score 1067.5; DB 11; Length 550;
 Best Local Similarity 42.7%; Pred. No. 6.1e-83;
 Matches 233; Conservative 87; Mismatches 185; Indels 41; Gaps 14;

Qy	18	LFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQDFDTLLLSGDGNTLY	77
		: : : : ::	
Db	15	LLLLLLLLLRTTTTRALG----PRISVPLGSEERLIRKFEAENISNYTALLLSQDGKTTY	70
Qy	78	VGAREAILALDIQDPGVP--RLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYN	135
		: : : : :: : : : ::: :	
Db	71	VGAREALFALNSNLSFLPGGEYQELL-WSADADRKQQCSFKGKDKPRDCQNYIKILLPLN	129
Qy	136	VTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVM--EGKGQSPFDPAHKHTAVLVDGML	193
		: : : : : : ::	
Db	130	SSHLLTCGTAAFSPLCAYIHIAFTLAQDEAGNVILEDGKGRCFPDPNFKSTALVVDGEL	189
Qy	194	YSGTMNIFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAA-----IPSTQVV	243
		: ::: :: : : :: : : : :	
Db	190	YTGTVSSFQGNPAISRQSSRPT-KTESSLNWL-QDPAFVASAYVPESLGSPIGDDDKI	247
Qy	244	YFFFEETASEFDFFERLHTRSARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQ-LPFN	302
		:: :: : : : : : : : :	
Db	248	YFFFSETGQEFEFFENTIVSRARVCKGDEGGERVLQQRWTSFLKAQLLCSRPDGFPFN	307
Qy	303	VIRHAVLL---PADSPTAPHIYAVFTSQWQVGTRSSAVCAFSLLDIERVFKGKYKELNK	359
		:: : : : : : : :	
Db	308	VLQDVFTLNPNPQDW-RKTLFYGVFTSQWHRGTTEGSAICVFTMNDVQKAFDGLYKKVNR	366
Qy	360	ETSRWTTYRGPETNPRPGSCSVGPS-----SDKALTFMKDHFLLMDEQVVGTPLL	408
		: : : : : : : : :	
Db	367	ETQQWYTETHQVPTPRPGACITNSARERKINSSLQLPDRVLNFKDHFLLMDGQVRSRLLL	426
Qy	409	VKSGVEYTRLAVETAQGLDGHS-HLVMYLGTGSLHKAVVSGDSSAHLVEEIQLFDPDE	467
		:: : : : : :: : : : :	
Db	427	LQPRARYQRVAVHRVPGL--HSTYDVLFLGTGDGRLHKAVTL-SSRVHIIIEELQIFPQGG	483

Qy 468 PVRNLQLAPTQGAVFVGFGSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLS 527
 ||:|| | | :: || :|| ||||:| :| ||:||||:|||| : |
 Db 484 PVQNLLLDSHGGLLYASSHSGVVQVPVANCSLYPTCGDCLLARDPYCAWTGSACRLASLY 543
 Qy 528 APNLNS 533
 |:| |
 Db 544 QPDLAS 549

RESULT 5

Q7Z5S4

ID Q7Z5S4 PRELIMINARY; PRT; 862 AA.
 AC Q7Z5S4;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE SEMA4D protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Strausberg R.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC054500; AAH54500.1; -.
 SQ SEQUENCE 862 AA; 96207 MW; 54C8EEB73B78938E CRC64;

Query Match 25.8%; Score 1041; DB 4; Length 862;
 Best Local Similarity 35.2%; Pred. No. 2.3e-80;
 Matches 271; Conservative 115; Mismatches 263; Indels 120; Gaps 27;

Qy 38 PMPRVRYAGDERRALSF--FHQKGLQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVP 95
 |:|: : | | : | |: : : | | | | : |:| |:| |:| |:| : : :
 Db 26 PIPRITW----EHREVHLVQFHEPDIYNYSALLSEDKDTLYIGAREAVFAVNALN--IS 79

Qy 96 RLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIE 155
 : : : | | : | |:| |:| | | | |:| |:| | | | | | | | | :
 Db 80 EKQHEVYWKVSEDKKAKCAEKGKSKQTECLNYIRVLQPLSATSLYVCGTNAFQPACDHLN 139

Qy 156 LQDSYLLPISEDKVMGKQSPFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQ 215
 | | | | | :| | | | | |:| |:| |:| |:| | | | | | | | | :
 Db 140 LTSFKFLGKNED----GKGRCPFDPAHSYTSMVDGELYSGTSYNFLGSEPIISRNSSHS 195

Qy 216 PVLKTDNFLRWLHHDASFVAA-----IPST-----QVYFFFEETASEFDFFERLHTSRV 265
 | |:| : : | | : : | | | | | : : | | | | | : |:| | : | :
 Db 196 P-LRTEYAI PWL-NEPSFVFADVIRKSPDSPDGEDDRVYFFFEVSVEYEFVFRVLIPRI 253

Qy 266 ARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQ-LPFNVIRHAVLLPADSPTAPHIYAVF 324
 | | | | | | | | : | | | | |:| |:| |:| |:| | | | | | | | | :
 Db 254 ARVCKGDQGGRLRTLQKKWTSFLKARLICSRPDSGLVFNVL RDVFVLRSPGLKVPVFYALF 313

Qy 325 TSQWQVGGTRSSAVCAFSLLDIERVFK-KGYKE---LNKETSRTTYRGPETNPRPGSCS 380
 | | : | | | | |:| | | | | | : : : : | | | | | |:| :
 Db 314 TP--QLNNVGLSAVCAYNLSTAEVFSHGKYMQSTTVEQSHTKWVRYNGPVPKPRPGACI 371

Qy 381 VGPS-----SDKALTFMKDHFLMDEQVV---GTPLLVKSGVEYTRLAVETAQGL 426
 : | | | | |:| | | | | | | | | | | | | | | | | : | |
 Db 372 DSEARAANYTSSNLNLPDKTLQFVKDHPLMDDSVTPIDNRPRLIKDVDNYTQIVVDRTQAL 431

Qy 427 DGHSHLVMYLGTTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQG--AVFVG 484
 | | : | |:| : | | |:| | | : | : : |:| | | | | | | | | : | : |
 Db 432 DGTVDVDMFVSTDRGALHKA-ISLEHAVHII EETQLFQDFEPVQTL LLSKKGNRFVYAG 490

Qy 485 FSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPE SRTCCLLSAPNLNSWKQDMERGNPE 544
 : | | : | | | : : | | | | | |:| | | | | | | | | | | |
 Db 491 SNSGVVQAPLAFCGKHGTCEDCVLARDPYCAWSPPTATCVALHQTESPSRGLIQEMSGDA 550

Qy 545 WACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPEASST 604
 | | | | | : : | | | | | | | | | | | | | | | | : | |
 Db 551 SVC-----PDKSKGSYRQHFFKHGGTAEKCSQKSNLARVFWKF-QNDVLKAESP 599

Qy 605 VY-----NGSLLLVQDGVGGLYQCWATE---NGFSYPVISYWVDSQDQTLALDPELAGI 656
 | | | | | : : : | | |:| | | : | | : |:| | | | | | | | : :
 Db 600 KYGLMGRKNLLIFNLSEGDSGVYQCLSEERVKNKTVFQVVAKHV-----LEVKV 649

Qy 657 PREHVKVPLTRV-SGGAALAAQSYWPHFVTVTVTLFALVLSGALIILVAS-----PLRA 709
 | : | | : | : | : : : : | | | | | | | | | | | | | |
 Db 650 PKPVVAPTLSVVQTEGSRIATK-----VLVASTQGSSPPTPA 686

Qy 710 LRARGKVQGCETLRPGEKAP-----LSREQHLQSPKECRTSASD 748
 : : | | | | | : | | : : | | | | | : | | | | : | |
 Db 687 VQATS--SGAITL-PPKPAPTGTSCPEKIVINTVPQLHSEKTMYLKSSD 732

RESULT 6

Q7Z3N1

ID Q7Z3N1

PRELIMINARY;

PRT;

681 AA.


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AC      Q7Z3N1;
DT      01-OCT-2003 (TrEMBLrel. 25, Created)
DT      01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Hypothetical protein DKFZp686A04130.
GN      DKFZP686A04130.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Human uterus;
RA      Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA      Han M., Wiemann S.;
RL      Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; BX537671; CAD97806.1; -.
KW      Hypothetical protein.
SQ      SEQUENCE      681 AA;  75401 MW;  9C4DAF83918BCDDA CRC64;

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      ::|   : | |||:   :| :|||: | ||   || : : :|   : |
Db      474 NASASCHVLPTGDL LLLVGTQQLGE-FQCWSLEEGFQQLVASYCPEVVEDGVADQTDEGGS 532

Qy      656 IPREHVKVPLTRVS----GGAALAAQQSYWPHFVTVTVLFALVLSGALIILVASPLRALR 711
      :|   | : :|||   | |: | :|||   |: : || | :   :: |:   :::
Db      533 VP---VIISTSRVSAPAGGKASWGADRSYWKFLVMCTLFVLAVLLPVLFLLYRHRNSMK 589

Qy      712 ARGKVQGCETLRPGEKAPLSREQHLQSPKEC 742
      |   | :: | : | :   :   || |
Db      590 VFLKQGECAVHP-KTCPV-----VLPPKTC 614

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RESULT 7

Q8BJC1

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ID   Q8BJC1          PRELIMINARY;          PRT;    799 AA.
AC   Q8BJC1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Semaphorin 4D precursor (Fragment).
GN   SEMA4D.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NOD; TISSUE=Thymus;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK088653; BAC40480.1; -.
DR   MGD; MGI:109244; Sema4d.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0007275; P:development; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003659; Plexin-like.
DR   InterPro; IPR002165; Plexin_repeat.
DR   InterPro; IPR001627; Sema.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF01437; PSI; 1.
DR   Pfam; PF01403; Sema; 1.
DR   SMART; SM00408; IGc2; 1.
DR   SMART; SM00423; PSI; 1.
DR   SMART; SM00630; Sema; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER      1      1
SQ   SEQUENCE      799 AA;  88814 MW;  415D3E687150A59A CRC64;

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Query Match          24.7%;  Score 995;  DB 11;  Length 799;
Best Local Similarity 40.2%;  Pred. No. 1.9e-76;
Matches 237;  Conservative 80;  Mismatches 212;  Indels 60;  Gaps 18;

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Qy 77 YVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNV 136
 |||||:|:: : : : : | : |||:| | | :|:| | :||| :
 Db 1 YVGAREAVFAVNALN--ISEKQHEVYWKVSEDKKSCKAEKGKSKQTECLNYIRVLQPLSR 58

Qy 137 THLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTAVLVDGMLYSG 196
 | | | | | | | | : | | | | | | : |||: ||||| :|:|:| | |||
 Db 59 TSLYVCGTNAFQPTCDHLNLTsfkflgksed----GKGRCPFDPAHSYTSVMVGGElySG 114

Qy 197 TMNFLGSEPILMRTLGSQPVLKTDNfLRWLHHDASFVAA-----IPSTQVVYFF 246
 | | | | | | | : | | :|: : | | :| | | | |||
 Db 115 TSYNFLGSEPIISRNSSSHSP-LRTEYAIPWL-NEPSFVFADVIQKSPDGEDEDKVVYFF 172

Qy 247 FEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQ-LPFNVIR 305
 | | : |::| :| | | | | | | | : | | | | :|||:|:|:| | | |:::
 Db 173 FTEVSVEYEFVFKLMI PRVARVCKGDQGGRLTLQKKWTSFLKARLICSKPDSGLVFNILQ 232

Qy 306 HAVLLPADSPTAPHIYAVFTSQWQVGTRSSAVCAFSLLDIERVF-KGKYKE---LNKET 361
 :| | | | | | | : | | | | :| : | | :| | : : :
 Db 233 DVFVLRAPGLKEPVFYAVFTP--QLNNVGLSAVCAYTLATVEAVFSRGKYMQSATVEQSH 290

Qy 362 SRWTTYRGPETNPRPGSCSVGPS-----SDKALTfMKDHFLMDEQVV---GTPL 407
 ::| | | | | | | : | | | | :| | | | | : | |
 Db 291 TKWVRYNGPVPTPRPGACIDSEARAANYTSSLNLPDKTLQFVKDHPMLDDSVTPIDNRPK 350

Qy 408 LVKSGVEYTRLAVETAQGLDGHSHLVMYLGT'TTGSfLHKAVVSGDSSAHLVEEIQLFDPDE 467
 |:| | | |::| : | | | : |::| | | :| | | | :|:| | | | |
 Db 351 LIKKDVNYTQIVVDRTQALDGTfyDVMFISTDRGALHKAVIL-TKEVHVIEETQLFRDSE 409

Qy 468 PVRNLQLAPTQGAVFV--GFSGGVWRVPRANCsvYESCVDCVLARDPHCAWDPEsRTCCL 525
 || | | : :| | | : | | : | | | : | | | | | | | | : |
 Db 410 PVLTLILLSSKGRKFVYAGSNGSVQAPLAFCEKHGSCEDCVLARDPYCAWSPAIKACVT 469

Qy 526 LSAPNLNS--WKQDMERGNPEWACASGPMsRSLRPQSRPQIIKEVLAVPNsILELPCPHL 583
 | : :| | | | | | | | | : : : | | |
 Db 470 LHQEEASSRGWIQDM-----SGDTSSCL--DKSKESfNQHFFKHGGTAELKCFQK 517

Qy 584 SALASYYW--SHG--PAAVPEASSTVYNGSLLLIVQDGVGGlyQCWATE 628
 | | | | :| | | : | : | | | :| | | :|
 Db 518 SNLARVVWKFQNGELKAASPKYGFVGRKHLfLIFNLSDGDSGVYQCLSEE 566

RESULT 8

Q810B2

ID Q810B2 PRELIMINARY; PRT; 722 AA.
 AC Q810B2;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Semaphorin M (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;

RA Jang W., Spilson S.V., Hua A., Roe B., Meisler M.H.;
 RT "Large-scale comparative sequence analysis of human and mouse genomic
 RT DNA reveals coding regions of three new genes."
 RL Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF038652; AAD02103.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 722 AA; 78612 MW; 716627589A9DB2D4 CRC64;

Query Match 21.9%; Score 882; DB 11; Length 722;
 Best Local Similarity 33.2%; Pred. No. 8.7e-67;
 Matches 238; Conservative 102; Mismatches 288; Indels 88; Gaps 24;

Qy	63	DFDTLLLSGDGNTLYVGAREAILALDIQDPG-VPRLKNMIPWPASDRKKSECAFKKKSNE	121
		:: : : ::: : : :	
Db	15	NYSALLVDPASHTLYVGARDSIFALTLPFSGEKPR---RIDWMVPETHRQNCR-KKGKKE	70
Qy	122	TQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPA	181
		: ::: : :: : : : : :	
Db	71	DECHNFIQILAIANASHLLTCGTFAFDPKCGVIDVSSFQQV----ERLESGRGKCPFEPA	126
Qy	182	HKHTAVLVDGMLYSGTMNIFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAI---	237
		: : : : : : : : : : : : :	
Db	127	QRSAAVMAGGVLYTATVKNFLGTEPIISRAVGRAEDWIRTETLSSWLNAPA-FVAAMVLS	185
Qy	238	-----PSTQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQ	290
		: : : : : :	
Db	186	PAEWGDEDGDDEIFFFTETSRVLDSYERIKVPRVARVCAGDLGGRKTLQQRWTTFLKAD	245
Qy	291	LLCTQP--GQLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIER	348
		: : : : :	
Db	246	LLCPGPEHGRASGVLQDMTELRPQPGAGTPLFYGIFSSQWE--GAAISAVCAFRPQDIRA	303
Qy	349	VFKGKYKELNKETSRWTTYRGPET-NPRPGSC-----SVGPS---SDKALTFMKDHF	396
		: : : : :	
Db	304	VLNGPFRELKHDCNRGLPVMNEVPQPRPGECITNNMKFQQFGSSLSLPDRVLTFFIRDHP	363
Qy	397	LMDEQVV---GTPLLVKSGVEYTRLAVETAQGLDGHSGLVLYLGTGSLHKAVVSGDSS	453
		: : : : : :	
Db	364	LMDRPVFPADGRPLLVTDTAYLRVVAHRVTSLSGKEYDVLYLGTEDGHLHRAVRIG-AQ	422
Qy	454	AHLVEEIQLFDPDEPVRNLQLAPTQGAVFVGFGSGGVWRVPRANC SVYESCVCVLARDPH	513
		: : : : : : : : : : : :	
Db	423	LSVLEDLALFPETQPVESMKL--YHDWLLVGSHTTEVTQVNTSNCGRQLQSCSECILAQDPV	480
Qy	514	CAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRPQSRPQIIKEVLAVPN	573
		: : : : : : : :	
Db	481	CAWS-FRLDACVAHAGEHRGMVQDIESADVSSLCPK-----EPGEHPVVFEPVATVG	532

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QY      574 SILELPCPHLSALASYWWSHGPAAVPEASSTVYNGSLLLLIVQDGVGGGLYQCWATENGFSY 633
      :: |||  || ||  | | | : |  | |  | : : | | | |  | | :
Db      533 HVV-LPCSPSSAWASCVW-HQPSGV--TSLTPRRDGLEVVVTPGAMGAYACECQEGGAAR 588

QY      634 PVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWPHFVTVTVLFLAL 693
      | :|  :|  :  | |  |  || |  |
Db      589 VVAAY-----SLVWGSQRGPANRAHTVV-----GAGLVG-----FFLG 621

QY      694 VLSGALIIIVAS-----PLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECR 743
      ||: :| :|:  | | || ||  |  |::  ||:: |
Db      622 VLAASLTLLLIGRRQRRRQRELLARDKVGLDLGAPPSGTTSSYSQDPPSPSPEDER 677

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RESULT 9

Q8QGU9

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ID      Q8QGU9          PRELIMINARY;          PRT;    756 AA.
AC      Q8QGU9;
DT      01-JUN-2002 (TrEMBLrel. 21, Created)
DT      01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Semaphorin 3F.
GN      SEMA3F.
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Watanabe Y., Nakamura H.;
RT      "Axon guidance of the trochlear nerve by Sema 3F along mid-hindbrain
RT      boundary.";
RL      Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AB072930; BAB88691.1; -.
DR      GO; GO:0007275; P:development; IEA.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003598; Ig_c2.
DR      InterPro; IPR003659; Plexin-like.
DR      InterPro; IPR001627; Sema.
DR      Pfam; PF00047; ig; 1.
DR      Pfam; PF01403; Sema; 1.
DR      SMART; SM00408; IGc2; 1.
DR      SMART; SM00423; PSI; 1.
DR      SMART; SM00630; Sema; 1.
DR      PROSITE; PS50835; IG_LIKE; 1.
KW      Immunoglobulin domain.
SQ      SEQUENCE    756 AA;  85196 MW;  C36754C02541ED88 CRC64;

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Query Match          21.2%;  Score 854.5;  DB 13;  Length 756;
Best Local Similarity 30.7%;  Pred. No. 2.2e-64;
Matches 245;  Conservative 123;  Mismatches 278;  Indels 151;  Gaps 34;

```

```

QY      32 GGGGQGPMPRVRYAGDERRALSFFHQKGL-----QDFDTLLLSGDGNTLYVG 79
      | | | |||:  |||  |  |:  ||  | : :|||
Db      22 GKDGVPPTPRVQ-----LSFKELKATGTAHFFNFLNSSDYRILLKDEDHDRMYVG 72

```

Qy 80 AREAILALDIQDPGVPR LKNMIPWPASDRKKSECAFKKKKSNETQCFNFIRVLVSYNVTHL 139
 ::: :|:|: | : | :| ||| :: || :| |||:: :| |||
 Db 73 SKDYVLSLDLHD--INREPLIIHWPASQQRIEECILSGKNSNGECGNFIRLIQPWNRTHL 130

Qy 140 YTCGTFAFSPACTFI----ELQDSYLLPISEDKVMEGKGQSPFDPAHKHTAVLVDGMLYS 195
 | ||| |::| | || : || | : ||: |||: :|| : |:: ||:
 Db 131 YVCGTGAYNPICAFINRGRKAQD-YIFYLEPDKLESGKGKCSYDPKVDTVSALINEELYA 189

Qy 196 GTMNNFLGSEPILMRTLGSQPVLKTDNF-LRWLHHDASFVAA--IPST-----QVYVFFF 247
 | :|:|:: : ||: | | :|| : ||| :| :|| | || : :|||
 Db 190 GVIYIDFMGTDAALFRMTGKQTAMRTDQYNSRWL-NDPAFVRAQLIPDSSERNDDKLYFFF 248

Qy 248 EETASEFDFFERLHTSRVARVCKNDVGGKLLQKKWTTFLKAQLLCTQPG----QLPFNV 303
 | :: : : ||: | :| || | | ||:||||:|:| | : |:
 Db 249 REKSADAPLSPGVY-SRIGRICLNDDGGHCCLVNKWSNFLKARLVCSVPGPDGIETHFDE 307

Qy 304 IRHAVLLPADSPTAPHIYAVFTSQQVVGTRSSAVCAFSLLDIERVFKGKYKELNKETSR 363
 :: : | ||||:: | : ||| :|: || || : :
 Db 308 LQDVFIQQTQDTKNPVIYAVFSASGSV--FKGSAVCVYSMADIRMFVFNRPFAHKEGPNYQ 365

Qy 364 WTTYRGPETNPRPGSCSVG---PS-----SDKALTFMKDHFMLDEQVVGTV---PLLVK 410
 | | | |||:| | || : : ||: | || | ||:|:
 Db 366 WMPYTGKMPYPRPGTCPPGTTFTPSMKSTKDYPEVINFMRSHPIMYHAVYPAHRQPLVVR 425

Qy 411 SGVEY--TRLAVETAQGLDGHSHLVMYLGT'TTGS LHKAVV-----SGDSSAHLVEEIQLF 464
 : | | | :||: || : |||| | :| : : :|||:|
 Db 426 TNVNYRFTTIAVDQVDAADGR-YEVLFLGTDRTGTVQKVI VLP RDDMETEELMLEEIEVFK 484

Qy 465 DPEPVRNLQLAPTQGA VFGVSGGVWRVPRANCSVY-ESCVD CVLARDPHCAWD PESRTC 523
 | |:: : : : :|| : | | : | || | :| || ||||:|||| : |
 Db 485 VPAPIKMMTISSKRQQLYVSSAVGVTHLALHRCDVYGEACADCCCLARDPYCAWD--GKAC 542

Qy 524 CLLSAPN-LNSWKQDMERGNPEWACASGPMSRSLRPQSRPQIIKEV-LAVPNSILELPCP 581
 || : | :||: ||| | | : : :| | | | |
 Db 543 SRYSA SKRRSRRQDVRHGNPMRQC-----RGYNSNANKNTVEAVQYGVGSTAFLECQ 596

Qy 582 HLSALASYW-----SHGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCWAT 627
 | | : | : | | : | | : | || :| ||| | ||
 Db 597 PRSPQATVKWLLQKDNSDRRKELRTEGGRAL-----RTEQG LLLRALQLSDSGLYSCTAT 651

Qy 628 ENGFSYPVISYWVDSQDQTLA-----LDPEL-----AGIPR-EHVKVPLTRVSGG 671
 || | : | | : || | || | || : : ||| |
 Db 652 ENNFKHTVTKV-----QLRVLAARAVHAVLLQGE LPPAALPGAPT PRYQDLLQLLTRPELG 707

Qy 672 AALAAQQSYW-----PHFVTVTVLFALVLSGALIIIVASPLRALRARGKVQGCETLRPG 725
 | : | | |||:|: :|
 Db 708 LLDQYCQGFWRPPAPGP-----PEPLAALKAK-ELQ-----D 738

Qy 726 EKAPLSREQHLQSPKEC 742
 :| | || | | : |
 Db 739 QKKPRSRRNH--PPESC 753

RESULT 10

Q8JIW9

ID Q8JIW9 PRELIMINARY; PRT; 774 AA.

AC Q8JIW9;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Semaphorin 3A.
 OS *Xenopus laevis* (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; *Xenopus*.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head;
 RA Tannahill D., Nielsen J., Regan A.G.;
 RT "Xenopus Semaphorin 3A."
 RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY030051; AAK38166.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR001005; Myb_DNA binding.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR PROSITE; PS00037; MYB_1; 1.
 SQ SEQUENCE 774 AA; 89319 MW; 3127FD2E0CCD5FA4 CRC64;

Query Match 21.0%; Score 847; DB 13; Length 774;
 Best Local Similarity 31.1%; Pred. No. 1e-63;
 Matches 227; Conservative 129; Mismatches 276; Indels 98; Gaps 27;

Qy 17 FLFQLLQLLLPTTTAGGGGQGMPRVRY---YAGDERRALSFFHQKGLQDFDTLLLSGDG 73
 ||| | : | | : : || : | : : | : : | :
 Db 9 FLF--LGVSLTTRLNCQNVKNNVPRRLRSYKEMVESNNLITFNGWPNSSSYNTFVLDEER 66

 Qy 74 NTLYVGAREAILALDIQDPGVPRLLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVS 133
 ||||| : | : : : | : : : || : : | : | || : || :
 Db 67 GRLYVGAKDHIFSFLAN--VKEFQKIL-WPVTNIRDECKWAGKDIVECANFIKVLKA 123

 Qy 134 YNVTHLYTCGTFAFSPACTFIEL-----QDSYLLPISEDKVME-GKGQSPFDPAHKHTAV 187
 || |||| || | | || : : : || : || | | : | : | : || : :
 Db 124 YNHTHLYACGTGAFHPVCTYIDVGHYPEQDNVFK--LEDSFFENGGRGKSPYDPKLLTASI 181

 Qy 188 LVDGMLYSGTMNIFLGSEPIRLMRTLGSPVLKTDNF-LRWLHHHDASFVAAI-----PS 239
 | : || |||| : : | : : |||| : : : || : | | : | : |
 Db 182 LIDGELYSGTAADFMRGRFAIFRTLGNHHPIRTEQHDNRWL-NDPRFIGAYLVPESDNPE 240

 Qy 240 TQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPG-- 297
 |||| | | : : : : : || : || : | ||||| : : : ||
 Db 241 DDKVYFFFRENAIDGHTGKATHARIGQLCKNDFGGHRSVLNKKWTTFLKARLICSVPGP 300

Qy 298 --QLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYK 355
 | : : : | | : : | | : | | | : : : | | | : | | | | |
 Db 301 GIDTHFDELQDVVLNMSKDKPNPVYAVFTTSSNI--FKGSACVMSYSLDIRRVFLGPYA 358
 Qy 356 ELNKETSRWTTYRGPETNPRPGSC-----SVGPSSDKALTFMKDHFMLDEQVV--- 403
 : : | : | | | | : | : : | : | | |
 Db 359 HRDGPNYQWVPFQGRVPYPRPGTCPRQTFGGFDSTKDLDPDEVIMFARSHPAMYNPVPFIN 418
 Qy 404 GTPLLVKSGVEY--TRLAVETAQGLDGHSHLVMYLGTTTGS LHKAV-----VSGDSSAHL 456
 | : : | : | | : : : | | : | | : | | : | | |
 Db 419 NRPIIIKTEVDYQFTQIVVDRVEAEDG-QYDVMFIGTDMGTILKVVSVPKETWTDLEEV 477
 Qy 457 VEEIQLFPDPEPVRNLQLAPTQGA VFGFSGGVWRVPRANCSVY-ESCVDCVLARDPHCA 515
 : | : : | : : : : | : : | | : | | : | : | | | : | |
 Db 478 LEEMTVFREPTAISAMEISTKQQQLYIGSSVGVSQLPLHRCDEVYKACAECCCLARDPYCA 537
 Qy 516 WDPESRTCCLLSAPNL--NSWKQDMERGNPEWACASGPMRSRLRPQSRP---QIIKE---VL 569
 | | | | : : | : | : | : | : | : | : | : | :
 Db 538 WDGSS---CSRYFPTAKRRTRRQDIRNGDPLTHCS-----DLQHQQDDPHRQSLEEKIY 588
 Qy 570 AVPNSILELPCPHLSALASYW-----SHGPAAVPEASSTVYNGSLLLLIVQDGVGGL 621
 | | | | | : | | : | | : | | : | : | :
 Db 589 GVENSSTFLECSPKSQRALVFWQFQKQNEEKKDEIKVDERKIKTEHGLLLRTLKKRDSGI 648
 Qy 622 YQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGA----- 672
 | | | | : | | | | | | | : | : | : |
 Db 649 YYCNAVEHGF-----QTL-LKVTLEIIDTEHLDELHKEDEGGDSHKHKEPS 695
 Qy 673 -ALAAQQSYW 681
 : : : | |
 Db 696 NSMSPTQKIW 705

RESULT 11

Q8TB71

ID Q8TB71 PRELIMINARY; PRT; 748 AA.
 AC Q8TB71;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC024220; AAH24220.1; -.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF00047; ig; 1.

DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 748 AA; 83034 MW; 587C53CB65AB4656 CRC64;

Query Match 20.3%; Score 817.5; DB 4; Length 748;
 Best Local Similarity 31.4%; Pred. No. 3.3e-61;
 Matches 208; Conservative 114; Mismatches 254; Indels 87; Gaps 24;

Qy	32	GGGGQGPMPRVRYAGDERRALSF-----FHQKGLQDF-----DTLLLSGDGNTLYV	78
		: : : :	
Db	20	GLGSAAPSP-----PRLRLSFQELQAWH--GLQTFSLERTCCYQALLVDEERGRLFV	69
Qy	79	GAREAILALDIQDPGVPRLNMI PWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTH	138
		: : : : : : : : : : : : :	
Db	70	GAENHVASLNLNLDN--ISKRAKKLAWPAPVEWREECNWAGKDIGTECMNFVKLLHAYNRTH	127
Qy	139	LYTCGTFAFSPACTFIEL---QDSYLLPISEDKVMGKGQSPFDPAHKHTAVLVDGMLYS	195
		: : : : : : : : : : :	
Db	128	LLACGTGAFHPTCAFVEVGHRAEELVRLDPGRIEDGKGKSPYDPRHRAASVLVGEELYS	187
Qy	196	GTMNNFLGSEPIILMRTLGSQPVLKTD-NFLRWLHHHDASFVAAI-----PSTQVVYFFF	247
		: : : : : : : : : : : :	
Db	188	GVAADLMGRDFTIFRSLGQRPSLRTEPHDSRWL-NEPKFVKVFWIPESENPDDDKIYFFF	246
Qy	248	EETASE-FDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQP---GQLPFNV	303
		: : : : : : : : :	
Db	247	RETAVEAAPALGRLSVSRVGQICRNDVGGQSRSLVNKWTTFLKARLVCSVPVGVEGDTHFDQ	306
Qy	304	IRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSR	363
		: : : : : : : : : : : :	
Db	307	LQDVFLSSRDHRTPLLYAVFSTSSIFQG---SAVCVYSMNDVRRRAFLGPFPAHKEGPMHQ	363
Qy	364	WTTYRGPEITNPRPGSC-----SVGPS SDKALTFMKDHF LMD EQVV---GTPLL VKS	411
		: : : : : : : :	
Db	364	WVS YQGRVPYPRPGMCP SKTFGTFSS TKDFPD DVIQFARNHPLMYSVLPTGGRPLFLQV	423
Qy	412	GVEY---TRLAVETAQGLDGHSHLV MYLGTTT GSLHK--AVVSG---DSSAHLVEEIQLFP	464
		: : : : : : : : : : :	
Db	424	GANYTFTQIAADRVAADGH-YDVLFIGTDVGTVLKVISVPKGSRPSAEGLLLEELHVFE	482
Qy	465	DPEPVRNLQLAPTQGA VFVGFSGGVWRVPRANCSVY-ESCVD CVLARDPHCAWD PESRTC	523
		: : : : : : : : : : : :	
Db	483	DSAAVTSMQISSKRHQLYVASRSAVAQIALHRCAAHGRVCTECCLARDPYCAWD---GVA	539
Qy	524	CLLSAPNLNS--WKQDMERGNPEWACASGPMRSRLRPQSRPQIIK-EVLAVPNSILELPC	580
		: : : : : : : :	
Db	540	CTRFQPSAKRRFRQDVRNGDPSTLCSG-----DSSRPALLEHKVFGVEGSSAFLEC	591
Qy	581	PHLSALASYW-----SHGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCWATENGFS	632
		: : : : : : : : :	
Db	592	EPRSLQARVEWTFQ RAGVTAHTQVLAEERTERTARGLLLRRLRRRDSGVYLCAAVEQGFT	651
Qy	633	YPV	635

Db |:
652 QPL 654

RESULT 12

Q8BMF6

ID Q8BMF6 PRELIMINARY; PRT; 777 AA.
AC Q8BMF6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Semaphorin 3D precursor homolog.
GN SEMA3D OR 4631426B19RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK031704; BAC27522.1; -.
DR MGD; MGI:1860118; Sema3d.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR001627; Sema.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
DR PROSITE; PS00038; HLH_1; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 777 AA; 89562 MW; B7204D82288B89CE CRC64;

Query Match 19.5%; Score 788; DB 11; Length 777;
Best Local Similarity 31.2%; Pred. No. 1.2e-58;
Matches 212; Conservative 111; Mismatches 279; Indels 78; Gaps 25;

Qy 11 WSLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGD---ERRALSFFHQKGLQDFDTL 67
| : | : : | | | : : | : : | : | | |
Db 22 WMMLIMTV-----LFLPVTET---SKQNIPRLKLTyKDLLSNTCIPFLGSSEGLDFQTL 73

Qy 68 LLSGDGNTLYVGAREAILALDIQDPGVPRLNKM--IPWPASDRKKSECAFKKKSNETQCF 125
| | : | : | : : | : | | | | : | | : |
Db 74 LLDEERGILLGAKDHVFLLSLVDLN----KNFKKIYWPAAKERVELCKLAGKDANAECA 129

Qy 126 NFIRVLVSYNVTHLYTCGTFAFSPACTFIEL---QDSYLLPISEDKVMGKGQSPFDPAH 182
| | | | | | | | : | | | | | : : : : : | : : | | |
Db 130 NFIRVLQPYNKTHVYVCGTGAHFPLCGYIDLGANKEELIFKLDTHNLESGRLKCPFDPPQ 189

Qy 183 KHTAVLVDGMLYSGTMNFLGSEPIILMRTLG---SQPVLKTD-NFLRWLHHDASFVAAI- 237
 Db 190 PFASVMTDEHLYSGTASDFLGKDTAFTRSLGLMQDHHSIRTDISEHHWL-NGAKFIGTFP 248

Qy 238 -----PSTQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQL 291
 Db 249 IPDTYNPDDDKIYFFFRESSQEGSTSDRSILSRVGRVCKNDVGGQRS LINKWTTFLKARL 308

Qy 292 LCTQPG----QLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIE 347
 Db 309 ICSIPGSDGADTHFDELQDIYLLPTRDERKPVVYGVFTTTSSI--FKGSAVCVYSMADIR 366

Qy 348 RVFKGKYKELNKETSRWTTYRGPETNPRPGSC-----SVGPSSDKALTFMKDHFL 397
 Db 367 AVFNGPYAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIRRHVPV 426

Qy 398 MDEQ---VVGTPLLVKSGVEY--TRLAVETAQGLDGHSHLVMYLGTTTGSLHKAVVSGDS 452
 Db 427 MYKSVYPVAGAPTFRINVDYRLTQIVVDHVVAEDG-QYDVMFLGTDIGTVLKVVVISKE 485

Qy 453 SAHL----VEEIQLFPDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRANCSVY-ESCVDCV 507
 Db 486 KWNMEEVVLEELQVFKHPTAILNMELSLKQQQLYVGSWDGLVQLSLHRCDTYGKACADCC 545

Qy 508 LARDPHCAWDPESTRCCLLSAP--NLNSWKQDMERGNPEWACASGPMSRSLRPQSRPQII 565
 Db 546 LARDPYCAWDGNA---CSRYAPTSKRARRQDVKYGDPITQC--WDIEDSISHETADE-- 598

Qy 566 KEVLAVPNSILELPCPHLSALASYW-----SHGPAAVPEAS--STVYNGSLLLIVQD 616
 Db 599 KVIFGIEFNSTFLECIPKSQQASVEWYIQRSGDEHREELKPDERIIKTDY-GLLIRSLQK 657

Qy 617 GVGGLYQCWATENGFSYPVI 636
 Db 658 KDSGMYCKAQEHTFIHTIV 677

RESULT 13

Q8BH34

ID Q8BH34 PRELIMINARY; PRT; 777 AA.
 AC Q8BH34;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Semaphorin 3D precursor homolog.
 GN SEMA3D OR 4631426B19RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Kidney, and Skin;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK028900; BAC26185.1; -.
 DR EMBL; AK052671; BAC35092.1; -.
 DR MGD; MGI:1860118; Sema3d.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR001092; HLH_basic.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS00038; HLH_1; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 SQ SEQUENCE 777 AA; 89548 MW; 5450D8D45D1BDABF CRC64;

Query Match 19.5%; Score 787; DB 11; Length 777;
 Best Local Similarity 31.2%; Pred. No. 1.5e-58;
 Matches 212; Conservative 111; Mismatches 279; Indels 78; Gaps 25;

QY 11 WSLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGD---ERRALSFFHQKGLQDFDTL 67
 | : | : : | | | : : | : : | : | | |
 Db 22 WMMLIMTV-----LFLPVETET---SKQNIPLRLKLTYSKDLLSNTCIPFLGSSEGLDFQTL 73

QY 68 LLSGDGNTLYVGAREAILALDIQDPGVPRKKNM--IPWPASDRKKSECAFKKKSNETQCF 125
 | | : | : | : : | : | | | | : : | : | : |
 Db 74 LLDEERGILLGAKDHVFLSLVDLN-----KNFKKIYWPAAKERVELCKLAGKDANAECA 129

QY 126 NFIRVLVSYNVTHLYTCGTFAPSPACTFIEL---QDSYLLPISEDKVMEGKGQSPFDPAH 182
 | | | | | | | | | | : | | | | | : | : : : : | : : | | |
 Db 130 NFIRVLQPYNKTHVYVCGTGAFHPLCGYIDLGANKEELIFKLDTHNLESGRLKCPFDPPQ 189

QY 183 KHTAVLVDGMLYSGTMNFLGSEPIMLRTLGL---SQPVLKTD-NFLRWLHHDASFVAAI- 237
 : | : | | | | : | | : : | : | : | : | : | : | : | : | : | :
 Db 190 PFASVMTDEHLYSGTASDFLGKDTAFTSLGLMQDHHSIRTDISEHHWL-NGAKFIGTFP 248

QY 238 -----PSTQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGKLLQKKWTTFLKAQL 291
 | : | | | | : : | : | | | | | | | : : | | | | | : |
 Db 249 IPDTYNPDDDKIYFFFRESSQEGSTSDRSILSRVGRVCKNDVGGQRLINKWTTFLKARL 308

QY 292 LCTQPG-----QLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIE 347
 : | : | | : : : | | | : | : | | : : : | | | : | : | |
 Db 309 ICSIPGSDGADTHFDELQDIYLLPTRDERNPVVYGVFTTTSSI--FKGSAVCVYSMADIR 366

QY 348 RVFKGKYKELNKETSRWTTYRGPETNPRPGSC-----SVGPSSDKALTFMKDHFL 397
 | | | | | | | | | | | | | | | | : : | : : | :
 Db 367 AVFNGPYAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDVISFIRRHVP 426

QY 398 MDEQ---VVGTPLLVKSGVEY--TRLAVETAQGLDGHSHLVMYLGTGSLHKAVVSGDS 452
 | : | | | : | : | : : | | : | : | | | : : | |
 Db 427 MYKSVYPVAGAPTFRINVDYRLTQIVVDHVVAEDG-QYDVMFLGTDIGTVLKVVSISKE 485

QY 453 SAHL-----VEEIQLFPDPEPVRNLQLAPTQGAFFVGFSGGVWRVPRANCSVY-ESCVDCV 507
 : : : | : | : | : | : | : | : | : | : | : | : | : | :
 Db 486 KWNMEEVLEELQVFKHPTAILNMELSLKQQQLYVGSWDGLVQLSLHRCPTYGKACADCC 545

QY 508 LARDPHCAWDPESTRCCLLSAP--NLNSWKQDMERGNPEWACASGPMRSRLRPQSRPQII 565
 |||||:|||| : | || : :||: |:| | : |: :: :
 Db 546 LARDPYCAWDGNA---CSRYAPTSKRRARRQDVKYGDPITQC--WDIEDSISHETADE-- 598
 QY 566 KEVLAVPNSILELPCPHLSALASYW-----SHGPAAVPEAS--STVYNGSLLLIVQD 616
 | : : : | | | || | | : | | | |: :|
 Db 599 KVIFGIEFNSTFLECI PKSQQASVEWYIQRSGDEHREELKPDERIIKTDY-GLLIRSLQK 657
 QY 617 GVGGLYQCWATENGFSYPVI 636
 |:| | | |:| : ::
 Db 658 KDSGMYCKAQEHTFIHTIV 677

RESULT 14

Q9NS98

ID Q9NS98 PRELIMINARY; PRT; 782 AA.
 AC Q9NS98; Q9H7Q3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Semaphorin sem2 (FLJ00014 protein).
 GN SEM2 OR FLJ00014.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Seki N., Hattori A., Hayashi A., Kozuma S., Muramatsu M., Miyajima N.,
 RA Saito T.;
 RT "Human semaphorin."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE OF 58-782 FROM N.A.
 RC TISSUE=Spleen;
 RA Ohara O., Nagase T., Kikuno R., Okumura K.;
 RT "The nucleotide sequence of a long cDNA clone isolated from human
 RT spleen."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB029496; BAA98132.1; -.
 DR EMBL; AK024425; BAB15715.1; -.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 SQ SEQUENCE 782 AA; 86700 MW; 85CB424874DF6663 CRC64;

Query Match 18.3%; Score 737; DB 4; Length 782;
 Best Local Similarity 28.9%; Pred. No. 3e-54;

Matches 236; Conservative 128; Mismatches 320; Indels 132; Gaps 33;

```
Qy      11 WSLGLFLFQLLQLLLPTTTAGGGGQGP-----MPRVRYAGD---ERRALSFFHQKGLQ 62
      | | | | |           | | | | : | : | | | : | : |
Db      10 WLLGGLLLH-----GGSSGSPSPGSPVRLRLSYRDLLSANRSAIFLGPQGS 56

Qy      63 DFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRILKNMIPWPASDRKKSECAFKKKSNET 122
      : : | : | : | : | : | : | : | : | : | : |
Db      57 NLQAMYLDEYRDLFLGGLDALYSLRL-DQAWPDPREVL-WPPQPGQREECVRKGRDPLT 114

Qy     123 QCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIEL--QDSYLLPISEDKVMGEGKQSPFDP 180
      : | | : | | : | | | | | | : : : | : | : | : |
Db     115 ECANFVRVLQPHNRTHLLACGTGAFQPTCALITVGHGRGEHVLHLEPGSVESGRGRCPHEP 174

Qy     181 AHKHTAVLVDGMLYSGTMNPNFLGSEPILMRTLGSQPVLTNDNFRWLHHDASFV--AAIP 238
      : : : | | : | : | | : : | : | : | : | : | | |
Db     175 SRPFASFIDGELYTGLTADFLGREAMI FRSGGPRPALRSDSD-QSLHDPREFVMAARIP 233

Qy     239 -----STQVVYFFFEETASEFD-FFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLL 292
      | | | | | | : | | | | | | : | | | | : |
Db     234 ENSDQDNDKVYFFSETVPSPDGGSNHVTVSRVGRVCVNDAGGQRVLVNKNWSTFLKARLV 293

Qy     293 CTQPG----QLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGRSSAVCAFSLLDIER 348
      | : | | : | : | | : : : | : | : | : |
Db     294 CSVPGPGGAETHFDQLEDVFLWPKAGKSLEVYALFSTVSAV--FQGFVAVCVYHMADIWE 351

Qy     349 VFKGKYKELNKETSRWTTYRGPETNPRPGSC-----SVGPSSDKALTFMKDH 395
      | | | : : : | | | | | | | | : | | : |
Db     352 VFNGPFAHRDGPQHGWGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKDYDPEVLQFARAH 411

Qy     396 FLMDEQV---VGTPLLVKSGV--EYTRLAVETAQGLDGHSHLVMYLGTTTGSLHKAVV-- 448
      | | | | | : | : : : | : : | | : | : | : | : |
Db     412 PLMFVWPVRPRHGRPVLVKTHLAQQQLHQIVVDRVEAEDG-TYDVIFLGTDSGSVLKVIALQ 470

Qy     449 ---SGDSSAHLVEEIQLFDPDPEPVRLQLAPTQGAVFVGFSGGVWRVPRANCSVY-ESCV 504
      | : : : | : | | : : : : : | | : | | : |
Db     471 AGGSAEPEEVVLEELQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCEITYGTACA 530

Qy     505 DCVLARDPHCAWDPESTRCCLLSAPNLNS---WKQDMERGNPEWAC-----ASGPMS 553
      : | | | | : | | | | : | : | : | | | | : :
Db     531 ECCLARDPYCAWDGAS---CTHYRPSLGKRRFRQDIRHGNPALQCLGQSQEEEEAVGLVA 587

Qy     554 RSLRPQSRPQIIKEVLAVPNISILELPCPHLSALASYW-----SHGPAAVPEASSTVY- 606
      : : | : : | | | : | | | : :
Db     588 ATM-----VYGTEHNSTFLECLPKSPQAAVRWLLQRPQDEGPDQVKTDERVLHT 636

Qy     607 -NGSLLLIVQDGVGGLYQCWATENGFSYPVIS----YWVDSQ-DQTLALDPE----- 652
      | | : | | | : | | | : | | | : |
Db     637 ERGLLFRRLSRFDAGTYTCTTLEHGFSQTVVRLALVVIVASQLDNLFPPEPKPEPPARG 696

Qy     653 -LAGIPREHVKVPLTRVSGGAALAAQQSY----WPHFVTVTVLFAVLVSGALIIIVASPL 707
      | | | : : : | | | | | | | | |
Db     697 GLASTPPKAWYKDILQLIGFANLPRVDEYCEVWCRTT-----ECSGCF-----RSRS 745

Qy     708 RALRARGKVQGCETLRPGKAPLSR--EQHLQSPKE 741
      | : | | | | | : | | | : | : | : |
Db     746 RGKQARGK--SWAGLELGKKMK-SRVHAEHNRTPRE 778
```

RESULT 15

Q96GX0

ID Q96GX0 PRELIMINARY; PRT; 635 AA.
 AC Q96GX0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC009113; AAH09113.1; -.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 635 AA; 70694 MW; D994099B476B9210 CRC64;

Query Match 18.3%; Score 736; DB 4; Length 635;
 Best Local Similarity 32.4%; Pred. No. 2.7e-54;
 Matches 180; Conservative 99; Mismatches 215; Indels 62; Gaps 19;

Qy 126 NFIRVLVSYNVTHLYTCGTFAPSPACTFIEL---QDSYLLPISEDKVMEGKGQSPFDPAH 182
 ||:::| :|| ||| ||| || | | |:| : :| : :: :|||:|:| |
 Db 2 NFKVLLHAYNRTHLLACGTGAFHPTCAFVEVGHRAEEPVLRLDPGRIEDGKGKSPYDPRH 61

Qy 183 KHTAVLVDGMLYSGTMNFLGSEPIILMRTLGSQPVLKTD-NFLRWLHHDASFVAAI----- 237
 : :||| ||| : :| : : | :| :| | :| : || : : ||
 Db 62 RAASVLVGEELYSGVAADLMGRDFTIFRSLGQRPSLRTEPHDSRWL-NEPKFVKVFWIPE 120

Qy 238 ---PSTQVVYFFFEETASE-FDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLC 293
 | :||| ||| | || ||| :|:|:|:|:| : | |||||:|:|
 Db 121 SENPDDDKIYFFFRETAEEAAPALGRLSVSRVGGQICRNDVGGQSRSLVNKWTTFLLKARLVC 180

Qy 294 TQP---GQLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVF 350
 : | | | : : : || : | :|||:| : | ||| :| : | |
 Db 181 SVPGVEGDTHFDQLQDVFLSSRDHRTPLLYAVFSTSSIFQG---SAVCVYSMNDVRRAF 237

Qy 351 KGKYKELNKETSRWTTYRGPETNPRPGSC-----SVGPSSDKALTFMKDHFLLMDEQ 401
 | : :| :|:| ||| | | | : | :| :| ||
 Db 238 LGPFAHKEGPMHQWVSYQGRVPYPRPGMCPSKTFGTFSSTKDFPDDVIQFARNHPLMYNS 297

Qy 402 VV---GTPLLKSGVEY--TRLAVETAQGLDGHSHLVMYLGTTTGS LHK--AVVSG---D 451
 |: | | | : | | | : | : | | | : | : | : | | | : | : | |
 Db 298 VLPTGGRPLFLQVGANYTFTQIAADRVAAADGH-YDVLFIGTDVGTVLKVISVPKGSRPS 356
 Qy 452 SSAHLVEEIQLFPDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRANCSVY-ESCVDCVLAR 510
 : | : | : : | | | : : | : : | : : | : : | : | | |
 Db 357 AEGLLLEELHVFEDSAAVTSMQISSKRHQLYVASRSAVAQIALHRCAAHGRVCTECCLAR 416
 Qy 511 DPHCAWDPESTRCTCLLSAPNLNS--WKQDMERGNPEWACASGPMSRSLRPQSRPQIIK-E 567
 | : | | | | | : | : | : | : | : | : | : | : | : | : | : | :
 Db 417 DPYCAWD---GVACTRFQPSAKRRFRQDVRNGDPSTLCSG-----DSSRPALLEHK 465
 Qy 568 VLAVPNSILELPCPHLSALASYW-----SHGPAAVPEASSTVYNGSLLLIVQDGVG 619
 | | | | | | | | : | : | : | : | : | : | : | : | : | : | :
 Db 466 VFGVEGSSAFLECEPRSLQARVEWTFQAGVTAHTQVLAEERTERTARGLLLRLRRRDS 525
 Qy 620 GLYQCWATENGFSYPV 635
 | : | | | | | : | :
 Db 526 GVYLCAAVEQGFTQPL 541

Search completed: May 5, 2004, 17:30:49
 Job time : 55 secs

OM protein - protein search, using sw model

Run on: May 5, 2004, 17:25:21 ; Search time 17 Seconds
 (without alignments)
 2330.905 Million cell updates/sec

Title: US-10-015-391A-277
 Perfect score: 4031
 Sequence: 1 MALPALGLDPWSLLGLFLFQ.....CRTSASDVADANNCLGTEVA 761

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	4031	100.0	761	1	SM4A_HUMAN	Q9h3s1 homo sapien
2	3280.5	81.4	760	1	SM4A_MOUSE	Q62178 mus musculu
3	1271.5	31.5	832	1	SM4B_HUMAN	Q9npr2 homo sapien
4	1198.5	29.7	782	1	SM4B_MOUSE	Q62179 mus musculu
5	1079.5	26.8	834	1	SM4C_MOUSE	Q64151 mus musculu
6	1062	26.3	861	1	SM4D_MOUSE	O09126 mus musculu
7	1043	25.9	862	1	SM4D_HUMAN	Q92854 homo sapien
8	984	24.4	837	1	SM4G_MOUSE	Q9wuh7 mus musculu
9	958	23.8	838	1	SM4G_HUMAN	Q9ntn9 homo sapien
10	919.5	22.8	770	1	SM4F_HUMAN	O95754 homo sapien
11	917	22.7	766	1	SMZ7_BRARE	Q9yhx4 brachydanio
12	904	22.4	777	1	SM4F_MOUSE	Q9z123 mus musculu
13	901.5	22.4	776	1	SM4F_RAT	Q9z143 rattus norv
14	880.5	21.8	860	1	SZ1A_BRARE	Q9w7j1 brachydanio
15	841	20.9	785	1	SM3F_MOUSE	O88632 mus musculu
16	840	20.8	772	1	SM3A_RAT	Q63548 rattus norv
17	838	20.8	772	1	SM3A_CHICK	Q90607 gallus gall

18	837.5	20.8	764	1	SMZ2_BRARE	Q9w6g6	brachydanio
19	837	20.8	772	1	SM3A_MOUSE	O08665	mus musculu
20	825.5	20.5	771	1	SM3A_HUMAN	Q14563	homo sapien
21	823.5	20.4	785	1	SM3F_HUMAN	Q13275	homo sapien
22	820	20.3	749	1	SM3B_HUMAN	Q13214	homo sapien
23	816.5	20.3	778	1	SZ1B_BRARE	Q9w686	brachydanio
24	802.5	19.9	751	1	SM3C_MOUSE	Q62181	mus musculu
25	793.5	19.7	777	1	SM3D_HUMAN	O95025	homo sapien
26	791.5	19.6	751	1	SM3C_CHICK	O42236	gallus gall
27	789.5	19.6	761	1	SM3D_CHICK	Q90663	gallus gall
28	784.5	19.5	748	1	SM3B_MOUSE	Q62177	mus musculu
29	782.5	19.4	751	1	SM3C_HUMAN	Q99985	homo sapien
30	723.5	17.9	1093	1	SM5B_HUMAN	Q9p283	homo sapien
31	700.5	17.4	775	1	SM3E_HUMAN	O15041	homo sapien
32	700.5	17.4	775	1	SM3E_MOUSE	P70275	mus musculu
33	695.5	17.3	1077	1	SM5A_MOUSE	Q62217	mus musculu
34	694	17.2	1093	1	SM5B_MOUSE	Q60519	mus musculu
35	679.5	16.9	886	1	SM6B_MOUSE	O54951	mus musculu
36	678.5	16.8	888	1	SM6A_MOUSE	O35464	mus musculu
37	677.5	16.8	1074	1	SM5A_HUMAN	Q13591	homo sapien
38	673	16.7	888	1	SM6B_HUMAN	Q9h3t3	homo sapien
39	672.5	16.7	887	1	SM6B_RAT	O70141	rattus norv
40	671	16.6	1030	1	SM6A_HUMAN	Q9h2e6	homo sapien
41	662	16.4	785	1	SM3E_CHICK	O42237	gallus gall
42	657.5	16.3	730	1	SM1A_SCHAM	Q26473	schistocerc
43	652.5	16.2	771	1	SM1A_DROME	Q24322	drosophila
44	630	15.6	930	1	SM6C_HUMAN	Q9h3t2	homo sapien
45	621.5	15.4	712	1	SM1A_CAEEL	Q17330	caenorhabdi

ALIGNMENTS

RESULT 1

SM4A_HUMAN

ID SM4A_HUMAN STANDARD; PRT; 761 AA.
AC Q9H3S1; Q8WUA9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Semaphorin 4A precursor (Semaphorin B) (Sema B).
GN SEMA4A OR SEMB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Seki N., Hattori A., Hayashi A., Kozuma S., Muramatsu M., Miyajima N.,
RA Saito T.;
RT "Human semaphorin B.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: INHIBITS AXONAL EXTENSION BY PROVIDING LOCAL SIGNALS TO
 CC SPECIFY TERRITORIES INACCESSIBLE FOR GROWING AXONS (By
 CC similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -!- SIMILARITY: Belongs to the semaphorin family.

CC -!- SIMILARITY: Contains 1 Sema domain.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

CC -----
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 CC -----

DR EMBL; AB029394; BAB20087.1; -.

DR EMBL; BC020974; AAH20974.1; -.

DR Genew; HGNC:10729; SEMA4A.

DR MIM; 607292; -.

DR InterPro; IPR003659; Plexin-like.

DR InterPro; IPR002165; Plexin_repeat.

DR InterPro; IPR001627; Sema.

DR Pfam; PF01437; PSI; 1.

DR Pfam; PF01403; Sema; 1.

DR SMART; SM00423; PSI; 1.

KW Signal; Transmembrane; Immunoglobulin domain; Multigene family;

KW Neurogenesis; Developmental protein; Glycoprotein.

FT SIGNAL 1 32 POTENTIAL.

FT CHAIN 33 761 SEMAPHORIN 4A.

FT DOMAIN 33 683 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 684 704 POTENTIAL.

FT DOMAIN 705 761 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 64 478 SEMA.

FT DOMAIN 496 548 PSI.

FT DOMAIN 573 631 IG-LIKE C2-TYPE.

FT DISULFID 580 624 BY SIMILARITY.

FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	135	135	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	496	496	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	607	607	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	293	328	CTQPGQLPFNVIRHAVLLPADSPTAPHIYAVFTSQW ->
FT				SAPSRGSCPSTSSATRSCSPILPQLPTSTQSSPPSG (IN
FT				REF. 1).
FT	CONFLICT	354	354	Y -> F (IN REF. 1).
SQ	SEQUENCE	761 AA;	83573 MW;	5BCB889AA32A2BB3 CRC64;

Query Match 100.0%; Score 4031; DB 1; Length 761;
 Best Local Similarity 100.0%; Pred. No. 9.8e-318;
 Matches 761; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG	60
Db	1	MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKG	60
Qy	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKS	120
Db	61	LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKS	120
Qy	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Db	121	ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDP	180
Qy	181	AHKHTAVLVDGMLYSGTMNIFLGSEPIMLRTLGSQPVLKTDNFLRWLHHDASFVAAPST	240
Db	181	AHKHTAVLVDGMLYSGTMNIFLGSEPIMLRTLGSQPVLKTDNFLRWLHHDASFVAAPST	240
Qy	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Db	241	QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLP	300
Qy	301	FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Db	301	FNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKE	360
Qy	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAV	420
Db	361	TSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAV	420
Qy	421	ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Db	421	ETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGA	480
Qy	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Db	481	VFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMER	540
Qy	541	GNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYYWSHGPAAVPE	600
Db	541	GNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYYWSHGPAAVPE	600
Qy	601	ASSTVYNGSLLLIVQDGVGGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660
Db	601	ASSTVYNGSLLLIVQDGVGGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREH	660

Qy 661 VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFLVLSGALIILVASPLRALRARGKVQGCE 720
 |||
 Db 661 VKVPLTRVSGGAALAAQQSYWPHFVTVTVLFLVLSGALIILVASPLRALRARGKVQGCE 720

Qy 721 TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA 761
 |||
 Db 721 TLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA 761

RESULT 2

SM4A_MOUSE

ID SM4A_MOUSE STANDARD; PRT; 760 AA.
 AC Q62178;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Semaphorin 4A precursor (Semaphorin B) (Sema B).
 GN SEMA4A OR SEMAB OR SEMB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NMRI; TISSUE=Brain;
 RX MEDLINE=95267431; PubMed=7748561;
 RA Pueschel A.W., Adams R.H., Betz H.;
 RT "Murine semaphorin D/collapsin is a member of a diverse gene family
 RT and creates domains inhibitory for axonal extension.";
 RL Neuron 14:941-948(1995).
 CC -!- FUNCTION: INHIBITS AXONAL EXTENSION BY PROVIDING LOCAL SIGNALS TO
 CC SPECIFY TERRITORIES INACCESSIBLE FOR GROWING AXONS.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED FROM DAY 10 IN THE EMBRYO. LOW
 CC LEVELS FOUND BETWEEN DAYS 10-12. EXPRESSION PEAKS ON DAY 13 WITH
 CC MODERATE LEVELS FROM THEN UNTIL BIRTH.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X85991; CAA59983.1; -.
 DR PIR; I48745; I48745.
 DR MGD; MGI:107560; Sema4a.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.

Db	479	GAVFAGFSGGIWRVPRANCSVYESCVDCVLARDPHCAWDPE SRLCSLLSG-STKPWKQDM	537
Qy	539	ERGNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAV	598
Db	538	ERGNPEWVCTRGP MARS PR RQSP PQLIKEVLTVPNSILELRCPHLSALASYHWSHGRAKI	597
Qy	599	PEASSTVYNGSLLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPR	658
Db	598	SEASATVYNGSLLLLLPQDGVGGLYQCVATENGYSYPVVSYWVDSQDQPLALDPELAGVPR	657
Qy	659	EHVKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALIILVASPLRALRARGKVQG	718
Db	658	ERVQVPLTRVGGGASMAAQRSYWPHFLIVTVLLAIVLLGVLTLLLASPLGALRARGKVQG	717
Qy	719	CETLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA	761
Db	718	CGMLPPREKAPLSRDOHLQPSKDHRTSASDVDADNNHLGAEVA	760

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: INHIBITS AXONAL EXTENSION BY PROVIDING LOCAL SIGNALS TO
 CC SPECIFY TERRITORIES INACCESSIBLE FOR GROWING AXONS (BY
 CC SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- CAUTION: Ref.3 sequence differs from that shown in position 709
 CC onward due to a frameshift.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB051532; BAB21836.1; -.
 DR EMBL; AL390080; CAB98204.1; -.
 DR EMBL; AL390081; CAB98205.1; -.
 DR EMBL; AL390082; CAB98206.1; -.
 DR EMBL; AK026133; BAB15372.1; ALT_FRAME.
 DR EMBL; BC010701; AAH10701.1; ALT_INIT.
 DR EMBL; BC017658; AAH17658.1; -.
 DR Genew; HGNC:10730; SEMA4B.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 KW Transmembrane; Immunoglobulin domain; Multigene family; Neurogenesis;
 KW Developmental protein; Glycoprotein; Signal; Polymorphism.
 FT SIGNAL 1 38 POTENTIAL.
 FT CHAIN 39 832 SEMAPHORIN 4B.
 FT DOMAIN 39 712 EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	713	733	POTENTIAL.
FT	DOMAIN	734	832	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	65	502	SEMA.
FT	DOMAIN	520	574	PSI.
FT	DOMAIN	599	658	IG-LIKE C2-TYPE.
FT	DOMAIN	753	776	PRO-RICH.
FT	DISULFID	606	651	BY SIMILARITY.
FT	CARBOHYD	64	64	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	91	91	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	160	160	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	405	405	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	520	520	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	625	625	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARIANT	792	792	S -> A.
FT				/FTid=VAR_010758.
FT	CONFLICT	160	160	N -> P (IN REF. 2).
FT	CONFLICT	565	565	E -> K (IN REF. 4; AAH10701).
SO	SEQUENCE	832 AA;	92192 MW;	29D58C1DDD5E1C6B CRC64;

Query Match 31.5%; Score 1271.5; DB 1; Length 832;
Best Local Similarity 39.1%; Pred. No. 1.4e-94;
Matches 304; Conservative 126; Mismatches 273; Indels 75; Gaps 27;

Qy	10	PWSLL----GLFLFQLLQLLL---PTTTAGGGGQGPMRVRYYAGDERRALSFHHQKGLQ	62
Db	10	PWGALPPRPPLLLLLLLLLLLLLLQPPPPTWA-----LSPRISLPLGSEERPFLRFEAHIS	63
Qy	63	DFDTLLLSGDGNTLYVGAREAILALDIQDPGPV--RLKNMIPWPASDRKKSECAFKKKS	120
Db	64	NYTALLLSRDGRTLYVGAREALFALSNNLSFLPGGEYQELL-WGADAEEKQQCSFKGKDP	122
Qy	121	ETQCENFIRVLVSYNVTHLYTCGTFAFSFACTFIELQDSYLLPISEDKVM--EGKGQSPF	178
Db	123	QRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCPF	182
Qy	179	DPAHKHTAVLVDGMLYSGTMNPNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVA--	236
Db	183	DPNFKSTALVVDGELYTGTVSSFGNDPAISRQSRLRPT-KTESSLNLW-QDPAFVASAY	240
Qy	237	IPST-----QVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLK	288
Db	241	IPESLGSLQGDDDKIYFFFSETGQEFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLK	300
Qy	289	AQLLCTQPGQ-LPFNVIRHAVLLPADSPTAPH-----IYAVFTSQWQVGGTRSSAVCAFS	342
Db	301	AQLLC SRPDDGF PFENVLQDVFTL---SPSPQDWDRDTLFYGVFTSQWHRGTTGSAVCVFT	357
Qy	343	LLDIERVFKGKYKELNKETSRTWTYRGPETNPRPGSCSVGPS-----SDKALT	391
Db	358	MKDVRQVRSGLYKEVNRETQQWYTVTHTPVPTPRPGACITNSARERKINSSLQLPDRV LNF	417
Qy	392	MKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSMLVYLGT TTGSLHKAVVSGD	451
Db	418	LKDHF LMDGQVRSRMLLLQPQARYQRVAVHRVPGLH-HTYDVLF LGTGDGR LHKA VSVG-	475
Qy	452	SSAHLVEEIQLPDPEPVRNLQLAPTQGA VFVGFSGGVWRVPRANCSVYESCVDCLARD	511

Db 476 PRVHIEELQIFSSGQPVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARD 535

Qy 512 PHCAWDPESTRCCLLSAPNL--NSWKQDMERGNPEWAC--ASGPMRSRLRPQSRPQIIKEV 568
 |:||| | | | | | |:| : : | || :| | | : :|

Db 536 PYCAWSGSSCKHVSLYQPQLATRPWIQDIEGASAKDLCSASSVVSPSFPVPTGE-KPCEQV 594

Qy 569 LAVPNSILELPCPHLSALASYWWSHGPAAVPEASS---TVYNGSLLLIVQDGVGGLYQCWA 626
 ||:: | || || |: | | | :| : | ||| :| :|||:

Db 595 QFQPNTVNTLACPLLSNLATRLWLRNGAPVNASASCHVLPTGDLILLVGTQQLGE-FQCWS 653

Qy 627 TENGFSYPVISYWVDSQDQTLALDPELAG--IPREHVKVPLTRVS----GGAALAAQQSYW 681
 | || | || : : :| : | :| | : :|| | | :| :|||

Db 654 LEEGFQQLVASYCPEVVEDGVADQTDGGSVP---VIISTSRVSAPAGGKASWGADRSYW 710

Qy 682 PHFVTVTVLFAL-VLSGALIILV--ASPLRALRARGKV-----QGCETLRPGEKAPLS 731
 | : : || | || | :| : : : :| : | : | | ||:

Db 711 KEFLVMCTLFVLAVLLPVLFLLYRHRNSMKVFLKQGECAVHPKTCPPVLPPEPTRPLN 768

RESULT 4

SM4B_MOUSE

ID SM4B_MOUSE STANDARD; PRT; 782 AA.

AC Q62179;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Semaphorin 4B (Semaphorin C) (Sema C) (Fragment).

GN SEMA4B OR SEMAC OR SEMC.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NMRI; TISSUE=Brain;

RX MEDLINE=95267431; PubMed=7748561;

RA Pueschel A.W., Adams R.H., Betz H.;

RT "Murine semaphorin D/collapsin is a member of a diverse gene family

RT and creates domains inhibitory for axonal extension.";

RL Neuron 14:941-948(1995).

RN [2]

RP INTERACTION WITH GIPC.

RX MEDLINE=99253973; PubMed=10318831;

RA Wang L.-H., Kalb R.G., Strittmatter S.M.;

RT "A PDZ protein regulates the distribution of the transmembrane

RT semaphorin, M-SemF.";

RL J. Biol. Chem. 274:14137-14146(1999).

CC -!- FUNCTION: INHIBITS AXONAL EXTENSION BY PROVIDING LOCAL SIGNALS TO

CC SPECIFY TERRITORIES INACCESSIBLE FOR GROWING AXONS.

CC -!- SUBUNIT: Interacts with GIPC PDZ domain.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- DEVELOPMENTAL STAGE: EXPRESSED FROM DAY 10 IN THE EMBRYO. LOW

CC LEVELS FOUND BETWEEN DAYS 10-12. EXPRESSION PEAKS ON DAY 13 WITH

CC MODERATE LEVELS FROM THEN UNTIL BIRTH.

CC -!- SIMILARITY: Belongs to the semaphorin family.

CC -!- SIMILARITY: Contains 1 Sema domain.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

CC -----
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 CC -----

DR EMBL; X85992; CAA59984.1; -.
 DR PIR; I48746; I48746.
 DR MGD; MGI:107559; Sema4b.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 KW Transmembrane; Immunoglobulin domain; Multigene family; Neurogenesis;
 KW Developmental protein; Glycoprotein.
 FT NON_TER 1 1
 FT DOMAIN <1 662 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 663 683 POTENTIAL.
 FT DOMAIN 684 782 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 16 453 SEMA.
 FT DOMAIN 471 525 PSI.
 FT DOMAIN 548 608 IG-LIKE C2-TYPE.
 FT DOMAIN 703 726 PRO-RICH.
 FT DISULFID 555 601 BY SIMILARITY.
 FT CARBOHYD 12 12 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 15 15 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 471 471 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 526 526 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 574 574 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 639 639 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 782 AA; 86823 MW; 627A81FC8F8F7AC8 CRC64;

Query Match 29.7%; Score 1198.5; DB 1; Length 782;
 Best Local Similarity 39.9%; Pred. No. 1e-88;
 Matches 275; Conservative 115; Mismatches 244; Indels 55; Gaps 22;

Qy 49 ERRALSFFHQKGLQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVP--RLKNMIPWPAS 106
 | | : | : : :: |||| || ||||| : ||: :| : :: | |
 Db 1 EERLIRKFEAENISNYTALLLSQDGKTLVVGAREALFALNSNLSFLPGGEYQELL-WSAD 59
 Qy 107 DRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISE 166
 :| :|:| | : | |:|:|:| :| :|| |||| |||| | :| : |
 Db 60 ADRKQQCSFKGKDPKRDCQNYIKILLPLNSSHLLTCGTAAFSPLCAYIHIASTLAQDEA 119
 Qy 167 DKVM--EGKGQSPFDPAHKHTAVLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFL 224
 |: :||| |||| | ||:| ||| ||:|:|:| |:| :|: |:| ||:| |
 Db 120 GNVILEDGKGHCPCFDPNFKSTALVVDGELYTGTVSSSQNDPAISRSQSSRPT-KTESSL 178

QY 225 RWLHHDSFVAAIPSTQ-----VYFFFEETASEFDFFERLHTSRVARVCKNDVG 274
 || | :|||: | : :||| || ||:|| | ||||| | |
 Db 179 NWL-QDPAFVASATSPEISLGSPIGDDDKIYFFFSETGQEFEEFFENTIVSRVARVCKGDEG 237

QY 275 GEKLLQKKWTTFLKAQLLCTQPGQ-LPFNVIRHAVLL---PADSPTAPHIYAVFTSQWQV 330
 ||::||:|:|:| ||||| ||:| |||:| | | | |||||
 Db 238 GERVLQQRWTSFLKAQLLCSRPDGFPFNVLQDVFTLNPNPQDWRKTLSTI-GVFTSQWHR 296

QY 331 GGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNPRPGSCSVGPS----- 384
 | | ||:| |:| |:| | | ||:|:| | :| | |||:| :
 Db 297 GTTEGSAICVFTMNDVQKAFDGLYKKVNRETQQWYTETHQVPTPRPGACITNSARERKIN 356

QY 385 -----SDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAVETAQGLDGHS-HLVMYLGT 438
 |: | |:| ||||| || ||:| | |:| | | | : |:| ||
 Db 357 SSLQLPDRVLNFLKDHFLMDGQVRSRLLLQLPRARYQRVAVHRVPGL--HSTDYDLFLGT 414

QY 439 TTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGAFFVGFSGGVWRVPRANCS 498
 | |||| | |:|:|:|:| |:|:| | | :| | | |||
 Db 415 GDGRHLKAVTL-SSRVHIIIEELQIFPQGPVQNLLLDSHGGLLYASSHSGVVQVPVANC 473

QY 499 VYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNS--WKQDMERGNPEWACASGPMSRSL 556
 :| :| ||:| ||||:| | : | |:| | | |:| : : | :
 Db 474 LYPTCGDCLLARDPYCAWTGSACRLASLYQPDLASRPWTQDIEGASVKELCKNSSYKARE 533

QY 557 RPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAPVEASS--TVYNGSLLLI- 613
 :| |:| ||:| || || || |:| | | | :| : | |||:
 Db 534 LVPGKP--CKQVQIQPNTVNTLACPLLSNLATRLWVHNGAPVNASASCRVLPTGDLILLVG 591

QY 614 VQDGVGGGLYQCWATENGFSYPVISYWVDSQDQ-TLALDPELAGIPREHVKVPLTRVS--- 669
 | |:| |:| |:| | || | || : : : : | | | : : ||
 Db 592 SQQGL-GVFQCWSIEEGFQQLVASYCPEVMEEGVMDQKNQRDGTG---VIINTSRVSAPA 647

QY 670 -GGAALAAQQSYWPHFVTVTVL--FALVL 695
 | : | :|| | |: : | ||:|
 Db 648 GGRDSWGADKSYWNEFLVMCTLFVFAMVL 676

RESULT 5

SM4C_MOUSE

ID SM4C_MOUSE STANDARD; PRT; 834 AA.
 AC Q64151;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Semaphorin 4C precursor (Semaphorin I) (Sema I) (Semaphorin C-like 1)
 DE (M-Sema F).
 GN SEMA4C OR SEMAI OR SEMACL1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Neonatal brain;
 RX MEDLINE=95385809; PubMed=7656991;
 RA Inagaki S., Furuyama T., Iwahashi Y.;
 RT "Identification of a member of mouse semaphorin family.";

RL FEBS Lett. 370:269-272(1995).
 RN [2]
 RP INTERACTION WITH GIPC.
 RX MEDLINE=99253973; PubMed=10318831;
 RA Wang L.-H., Kalb R.G., Strittmatter S.M.;
 RT "A PDZ protein regulates the distribution of the transmembrane
 RT semaphorin, M-SemF.";
 RL J. Biol. Chem. 274:14137-14146(1999).
 CC -!- SUBUNIT: Interacts with GIPC PDZ domain.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: EXPRESSED WIDELY IN THE NERVOUS TISSUES DURING
 CC DEVELOPMENT. PREDOMINANTLY IN THE DEVELOPING BRAIN AND SPINAL
 CC CORD.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -----
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 CC -----
 DR EMBL; S79463; AAB35184.1; -.
 DR PIR; S66498; S66498.
 DR MGD; MGI:109252; Sema4c.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Signal; Transmembrane; Immunoglobulin domain; Multigene family;
 KW Neurogenesis; Developmental protein; Glycoprotein.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 834 SEMAPHORIN 4C.
 FT DOMAIN 21 664 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 665 685 POTENTIAL.
 FT DOMAIN 686 834 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 53 481 SEMA.
 FT DOMAIN 499 552 PSI.
 FT DOMAIN 557 645 IG-LIKE C2-TYPE.
 FT DOMAIN 678 687 POLY-LEU.
 FT DOMAIN 709 774 PRO-RICH.
 FT DOMAIN 831 834 BINDS TO GIPC.
 FT DISULFID 578 628 BY SIMILARITY.
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 310 310 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 565 565 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 834 AA; 92556 MW; 6868BB5BF571482D CRC64;

Query Match 26.8%; Score 1079.5; DB 1; Length 834;
 Best Local Similarity 35.4%; Pred. No. 4.7e-79;
 Matches 271; Conservative 115; Mismatches 242; Indels 137; Gaps 25;

Qy 39 MPRVRYAGDERRALSFFHQKGLQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLK 98
 :|| :| : | | | :|| | | : | | | | | : | : : | :
 Db 28 VPRKTVSSGELVTVVRFSQTGIQDFLTTLTEHSGLLYVGAREALFAFSVE---ALELQ 84

Qy 99 NMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQD 158
 | | | | | | | | | | | | | | | | | | | | | :
 Db 85 GAISWEAPAEKKIECTQKGKSNQTECFNFIRFLQPYNSSHLYVCGTYAFQPKCTYINM-- 142

Qy 159 SYLLPISEDKVMEGKGQSPFDPAHKHTAVLVDGMLYSGTMNNFLGSEPILMRTLGSQPVL 218
 : : : | | : | | | | | | | | | | | | | | : : :
 Db 143 -LFTFLDRAEFEDGKGKCPYDPAKGHTGLLVDGELYSATLNNFLGTEPVILRYMGTHHSI 201

Qy 219 KTDNFLRWLHHDasFV--AAIPST-----QVYFFFEETASEFDFFERLHTSRVARV 268
 || : | : | | : | : : | | | | | | | : | : : | | | |
 Db 202 KTEYLAFWL-NEPHFVGSFAVPESVGSFTGDDDKIYFFFSERAVEYDCYSEQVVARVARV 260

Qy 269 CKNDVGGEKLLQKKWTTFLKAQLLCTQPG-QLPFNVIRHAVLLPADSPTAPHIYAVFTSQ 327
 || : | : | | | | | | | | | : | : : | : : | : | : :
 Db 261 CKGDMGGARTLQKKWTTFLKARLVCSAPDWKVYFNQLKAVHTLRGASWHNTTFFGVFQAR 320

Qy 328 WQVGGRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNPRPGSC-----SV 381
 | | | | : | | : | | | | | | : : : | | | : | | | |
 Db 321 W--GDMDLSAVCEYQLEQIQVFEGPYKEYSEQAQKWARYTDPVPSRPGSCINNWHDRN 378

Qy 382 GPSS-----DKALTFMKDHFLLMDEQV---VGTPLLVKSGVEYTRLAVETAQGLDGHSHLV 433
 | : | | | | | | : | | | : | | | | : | : : | | | : : |
 Db 379 GYTSSLELPDNTLNFIIKKHPLMEDQVKPRLGRPLLVKKNNTNFTHVVADRVPGLDGATYTV 438

Qy 434 MYLGT'TTGS LHKAVVSGDSSAHLVEEIQLFPDPEPVRLQLAPTQGA VFGVFGSGGVWRVP 493
 : : : | | | | | | | : | | | : | | | : | : : : | : : :
 Db 439 LFIGTGDGWLLKAVSLG-PWIHMVEELQVF-DQEPVESLVLSQSKKVL FAGSRSQLVQLS 496

Qy 494 RANCSVYESCVDCVLARDPHCAWDPEsrTCCLLSA-----PNLNSWKQDMERGN 542
 | : | : | | | | | | : | | : : | : : | : | : | : |
 Db 497 LADCTKYRFCVDCVLARDPYCAWNVNTSRCVATTSGRSGSFLVQHVANLDTSKMCNQYG- 555

Qy 543 PEWACASGPMSRSLRPQSRPQIIKEVLAVPNSI-----LELPCPHLSA-LASYWWSHG 594
 | : | : : | : | | | | | | : | | : | : | : | : |
 Db 556 -----IKKVR SIPKNITVSGTDLVLPCL-HLSSNLAAHAWTFG 592

Qy 595 PAAVP--EASSTVYNGSLLLIV-----QDGVGGLYQCWATENGFSYPVISYW---VDSQDQ 645
 : | : | : | : | : | | | : | : | | | | | |
 Db 593 SQDLPAEQPGSFLYDTGLQALVMAAQSRHSGPYRCYSEEQGT RLAAESYLVA VVAGSSV 652

Qy 646 TLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGA----LII 701
 || : | : | : | : | | | : | | | | : :
 Db 653 TL-----EARAPLENLG-----LVWLAVVALGAVCLVLLL 682

Qy 702 LVASPLRALRARGKVQGCETLRPGKA-----PLSREQHLQSP 739

Db 683 LVLSLRRRLR-----EELEKGAKASERTLVYPLELPKEPASP 719

RESULT 6

SM4D_MOUSE

ID SM4D_MOUSE STANDARD; PRT; 861 AA.
AC O09126;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Semaphorin 4D precursor (Semaphorin J) (Sema J) (Semaphorin C-like 2)
DE (M-Sema G).
GN SEMA4D OR SEMAJ OR SEMACL2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=97125976; PubMed=8969198;
RA Furuyama T., Inagaki S., Kosugi A., Noda S., Saitoh S.-I., Ogata M.,
RA Iwahashi Y., Miyazaki N., Hamaoka T., Tohyama M.;
RT "Identification of a novel transmembrane semaphorin expressed on
RT lymphocytes."
RL J. Biol. Chem. 271:33376-33381(1996).
CC -!- FUNCTION: MAY PLAY A FUNCTIONAL ROLE IN THE IMMUNE SYSTEM, AS WELL
CC AS IN THE NERVOUS SYSTEM.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN LYMPHOID TISSUES,
CC ESPECIALLY IN THE THYMUS, AS WELL AS IN THE NERVOUS TISSUES.
CC -!- SIMILARITY: Belongs to the semaphorin family.
CC -!- SIMILARITY: Contains 1 Sema domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -----
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CC -----
DR EMBL; U69535; AAC52964.1; -.
DR MGD; MGI:109244; Sema4d.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR InterPro; IPR001627; Sema.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF01437; PSI; 1.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.

DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal; Transmembrane; Immunoglobulin domain; Multigene family;
KW Neurogenesis; Developmental protein; Glycoprotein.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 861 SEMAPHORIN 4D.
FT DOMAIN 24 733 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 734 754 POTENTIAL.
FT DOMAIN 755 861 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 50 482 SEMA.
FT DOMAIN 502 551 PSI.
FT DOMAIN 555 636 IG-LIKE C2-TYPE.
FT DISULFID 576 624 BY SIMILARITY.
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 379 379 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 861 AA; 95714 MW; 533CD6D271A6D79B CRC64;

Query Match 26.3%; Score 1062; DB 1; Length 861;
Best Local Similarity 39.8%; Pred. No. 1.3e-77;
Matches 259; Conservative 92; Mismatches 232; Indels 68; Gaps 21;

Qy 15 GLFLFQLLQLLLPTTTAGGGGQGPMRVRYYAGDERRALSFFHQKGLQDFDTLLLSGDGN 74
| | | | | : : | | | : : : : | : | | : : : | : | :
Db 9 GLFL--ALVVVLRTAVA----FAPVPRLTWEHGEV--GLVQFHKPGIFNYSALLMSKD 60

Qy 75 TLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSNETQCFNFIRVLVSY 134
| | | | | : : : : : : : | : | | : | | : | : | : | :
Db 61 TLYVGAREAVFAVNALN--ISEKQHEVYWKVSEDKKSKCAEKGKSKQTECLNYIRVLQPL 118

Qy 135 NVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDPAHKHTAVLVDGMLY 194
: | | | | | | | : | | | | | : | | | | : | : | : | :
Db 119 SSTSLYVCGTNAFQPTCDHLNLTSEKFLGKSED----GKGRCPPDPAHSYTSVMVGELY 174

Qy 195 SGTMMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAA-----IPSTQVVY 244
| | | | | : | | : : : : | : : | | | : | :
Db 175 SGTSYNFLGSEPIISRNSHSP-LRTEYAIPWL-NEPSFVFADVIQKSPDGPEGEDDKVY 232

Qy 245 FFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQ-LPFNV 303
| | | : : : : | | | | | | : | | | : : : : | : | :
Db 233 FFFTEVSVEYEFVFKLMIPRVARVCKGDQGGRLTLQKKWTSFLKARLICSKPDSGLVFN 292

Qy 304 IRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVF-KGKYKE---LNK 359
: : : | | | | | : | | | : : | : | : : : : : :
Db 293 LQDVFVLRAPGLKEPVFYAVFTP--QLNNVGLSAVCAYTLATVEAVFSRGKYMQSATVEQ 350

Qy 360 ETSRWTTYRGPETNPRPGSCSVGPS-----SDKALTFMKDHFILMDEQVV---GT 405
: : | | | | : : : : | | | : | | : | : | : | :
Db 351 SHTKWVRYNGPVPTPRPGACIDSEARAANYTSSLNLDPDKTLQFVKDHPLMDDSVTPIDNR 410

Qy 406 PLLVKSGVEYTRLAVETAQGLDGHSHLVMYLGTGTTGSLHKAVVSGDSSAHLVEEIQLFDP 465
| : | | | : : | | | : : : | : | : : : : : : :
Db 411 PKLIKDVNYTQIVVDRTOALDGTFFYDMFISTDRGALHKAVIL-TKEVHVIEETQLFRD 469

Qy 466 PEPVRNLQLAPTQGAVFV--GFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPE\$RTC 523
 ||| | |: |: || | : || : | | | : || ||||| |: || | : |
 Db 470 FEPVLTLTLLSSKKGRKFVYAGSNSGVVQAPLAFCEKHGSCEDCVLARDPYCAWSPA\$KAC 529
 Qy 524 CLL\$APN\$LN\$--WKQDMERGNPEWACASGPM\$R\$R\$PQ\$R\$PQ\$IIKEVLAVPN\$ILELPCP 581
 | | :| | ||| || | | : : : || |
 Db 530 VTLHQEEASSRGW\$IQDM-----SGDTSSCL--DK\$KESFNQHFFKHGGTAELKCF 577
 Qy 582 HLSALASYYW--SHG--PAAVPEASSTVYNG\$LL\$LLIVQDGVGGLYQCWATE 628
 | || | :| || |: | : || |: ||| : |
 Db 578 QKSNLARVVWKFQNGELKAASPKYGFVGRKHLLIFN\$SDGDSGVYQCLSEE 628

RESULT 7

SM4D_HUMAN

ID SM4D_HUMAN STANDARD; PRT; 862 AA.
 AC Q92854;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Semaphorin 4D precursor (Leukocyte activation antigen CD100) (BB18)
 DE (A8) (GR3).
 GN SEMA4D OR CD100.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RX MEDLINE=97030273; PubMed=8876214;
 RA Hall K.T., Boumsell L., Schultze J.L., Boussiotis V.A., Dorfman D.M.,
 RA Cardoso A.A., Bensussan A., Nadler L.M., Freeman G.J.;
 RT "Human CD100, a novel leukocyte semaphorin that promotes B-cell
 RT aggregation and differentiation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:11780-11785(1996).
 CC -!- FUNCTION: MAY PLAY A FUNCTIONAL ROLE IN THE IMMUNE SYSTEM, AS WELL
 CC AS IN THE NERVOUS SYSTEM. INDUCES B CELLS TO AGGREGATE AND
 CC IMPROVES THEIR VIABILITY IN VITRO.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN SKELETAL MUSCLE,
 CC PERIPHERAL BLOOD LYMPHOCYTES, SPLEEN, AND THYMUS AND ALSO
 CC EXPRESSED AT LOWER LEVELS IN TESTES, BRAIN, KIDNEY, SMALL
 CC INTESTINE, PROSTATE, HEART, PLACENTA, LUNG, AND PANCREAS BUT NOT
 CC IN COLON OR LIVER.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD100 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd100.htm".
 CC -----
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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; U60800; AAC50810.1; -.
DR Genew; HGNC:10732; SEMA4D.
DR MIM; 601866; -.
DR GO; GO:0006916; P:anti-apoptosis; TAS.
DR GO; GO:0007155; P:cell adhesion; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR InterPro; IPR001627; Sema.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF01437; PSI; 1.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal; Transmembrane; Immunoglobulin domain; Multigene family;
KW Neurogenesis; Developmental protein; Glycoprotein.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 862 SEMAPHORIN 4D.
FT DOMAIN 22 734 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 735 755 POTENTIAL.
FT DOMAIN 756 862 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 50 482 SEMA.
FT DOMAIN 502 551 PSI.
FT DOMAIN 554 636 IG-LIKE C2-TYPE.
FT DISULFID 576 624 BY SIMILARITY.
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 379 379 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 862 AA; 96149 MW; 7B18EFEA98789371 CRC64;

Query Match 25.9%; Score 1043; DB 1; Length 862;
Best Local Similarity 35.2%; Pred. No. 4.4e-76;
Matches 271; Conservative 115; Mismatches 263; Indels 120; Gaps 27;

Qy 38 PMPRVRYAGDERRALSF--FHQKGLQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVP 95
|:|:|: | | : ||: : :: |||| | :|||:||||: |: : :
Db 26 PIPRITW----EHREVHLVQFHEPDIYNYSALLLSEDKDTLYIGAREAVFAVNALN--IS 79

Qy 96 RLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIE 155
: : : | |: ||: || | || :|: | :||| : | || ||| || ||| :
Db 80 EKQHEVYWKVSEDKKAKCAEKGKSKQTECLNYIRVLQPLSATSLYVCGTNAFQACDHLN 139

Qy 156 LQDSYLLPISEDKVMEGKGQSPFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQ 215

Db	140	LTSFKFLGKNED----GKGRCPFDPAHSYTSVMVDGELYSGTSYNFLGSEPIISRNSHS	195
Qy	216	PVLKTDNFLRWLHHDASFVAA-----IPST-----QVVYFFFEETASEFDEFFERLHTSRV	265
Db	196	P-LRTEYAIPWL-NEPSFVFADVIRKSPDSPDGEDDRVYFFFTVEVSVEYEFVFRVLIPRI	253
Qy	266	ARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQ-LPFNVIRHAVLLPADSPTAPHIYAVF	324
Db	254	ARVCKGDQGGRLRTLQKKWTSFLKARLICSRPDSGLVFNVLRDVFLRSPGLKVPVFYALF	313
Qy	325	TSQWQVGGTRSSAVCAFSLLDIERVFK-GKYKE---LNKETSRTTYRGPETNPRPGSCS	380
Db	314	TP--QLNNVGLSAVCAYNLSTAEVFSHGKYMOSTTVEQSHTKWVRYPVVKPRPGACI	371
Qy	381	VGPS-----SDKALTFMKDHFLMDEQVV---GTPLLKSGVEYTRLAVETAQGL	426
Db	372	DSEARAANYTSSLNLPDKTLQFVKDHPLMDDSVTPIDNRPRLIKDVNYTQIVVDRTQAL	431
Qy	427	DGSHSLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQG--AVFVG	484
Db	432	DGTVDVDMFVSTDRGALHKA-ISLEHAVHIIETQLFQDFEPVQTLSSKKGNRFVYAG	490
Qy	485	FSGGVWRVPRANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPE	544
Db	491	SNSGVVQAPLAFCGKHGTCEDCVLARDPYCAWSPPTATCVALHQTESPSRGLIQEMSGDA	550
Qy	545	WACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPEASST	604
Db	551	SVC-----PDKSKGSYRQHFFKHGGTAELKCSQKSNLARVFWKF-QNGVLKAESP	599
Qy	605	VY-----NGSLLLIVQDGVGGLYQCWATE---NGFSYPVISYWVDSQDQTLALDPELAGI	656
Db	600	KYGLMGRKNLLIFNLSEGDSGVYQCLSEERVKNKTVFQVVAKHV-----LEVKKV	649
Qy	657	PREHVKVPLTRV-SGGAALAAQQSYWPHFVTVTVLFLALVLSGALIIIVAS-----PLRA	709
Db	650	PKFVVAPTLSVVQTEGSRIATK-----VLVASTQGS SPPTPA	686
Qy	710	LRARGKVQGCETLRPGEKAP-----LSREQHLQSPKECRTSASD	748
Db	687	VQATS--SGAITL-PPKPAPTGTSCPEKIVINTVPQLHSEKTMYLKSSD	732

RESULT 8

SM4G_MOUSE

ID SM4G_MOUSE STANDARD; PRT; 837 AA.
AC Q9WUH7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Semaphorin 4G precursor.
GN SEMA4G.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=99425180; PubMed=10495281;
 RA Li H., Wu D.K., Sullivan S.L.;
 RT "Characterization and expression of sema4g, a novel member of the
 RT semaphorin gene family.";
 RL Mech. Dev. 87:169-173(1999).
 CC -!- FUNCTION: MAY PLAY A ROLE IN AXON GUIDANCE.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: BRAIN, SPINAL CORD, AND SEVERAL SENSORY ORGANS
 CC AS WELL AS SPECIFIC POPULATIONS OF PROJECTION NEURONS.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED EARLY IN DEVELOPMENT.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -----
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 CC -----
 DR EMBL; AF134918; AAD30541.1; -.
 DR MGD; MGI:1347047; Sema4g.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Signal; Transmembrane; Immunoglobulin domain; Multigene family;
 KW Neurogenesis; Developmental protein; Glycoprotein.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 837 SEMAPHORIN 4G.
 FT DOMAIN 18 673 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 674 694 POTENTIAL.
 FT DOMAIN 695 837 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 56 487 SEMA.
 FT DOMAIN 505 556 PSI.
 FT DOMAIN 565 647 IG-LIKE C2-TYPE.
 FT DOMAIN 563 566 POLY-PRO.
 FT DOMAIN 762 773 POLY-PRO.
 FT DISULFID 582 630 BY SIMILARITY.
 FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 540 540 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 596 596 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 837 AA; 92378 MW; 5C6E9C9C8A545EB1 CRC64;

Query Match 24.4%; Score 984; DB 1; Length 837;
Best Local Similarity 34.0%; Pred. No. 2.5e-71;
Matches 276; Conservative 106; Mismatches 287; Indels 142; Gaps 30;

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Qy      11 WSLGLFLFQLLQLLLPTTTAGGGGQGPMRVRYYAGDERRALSF-----FHQKG-LQD 63
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2 WGRWLPLLFSFL-----TVTAVPGPSLRRPS-RELDATPRLTISYEELSQIRHFKGQTQN 55

Qy      64 FDTLLLSGDGNTLYVGAREAILAL---DIQDPGVPRLNMIWPWASDRKKSECAFKKKSN 120
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      56 YSTLLLEEASERLLVGARGALFSLSARDIRD----RTHKEIHWEASPEMQSKCHQKGKNN 111

Qy     121 ETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP 180
      : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     112 QTECFNHVRFLQRLNATHFYACGTHAFQPLCAID-AETFILPTSFE---EGKEKCPYDP 167

Qy     181 AHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFV----- 234
      | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     168 ARGFTGLIIDGGLYTATRYEF-RSIPDIRSRHPHSLRTEEAPMHWL-NDAEFVFSVLVR 225

Qy     235 ----AAIPSTQVVYFFF---EETASEFDDFFERLH-TSRVARVCKNDVGGEKLLQKKWTF 286
      : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     226 ESKTSAVGDDDKIYFFFMEREESSTQSRSSSHRVARVARVCKGDLGGKKILQKKWTSF 285

Qy     287 LKAQLLCTQPQLPFNVIRHAVLLPADSPTAPIYAVF--TSQWQVGGTRSSAVCAFSLL 344
      | | | : | | | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     286 LKARLICHIP---QYETLRGVCSLNADTSSHTHFYAVFTLTQWKT--LEASAICRYDLA 340

Qy     345 DIERVFKGKYKELNKETSRWTTYRGPETNPRPGSC-----SVGPS SDK-----ALTFMK 393
      : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     341 EIQAVFTGPFMEYQDGARRWGRYEGGVPEPRPGSCITDSLRSRGYNSSQDLPSLVLD FVK 400

Qy     394 DHFLMDEQVV---GTPLLVKSGVEYTRLAVETAQGLDGHSHLVMYLGTTTGSLHKAVVSG 450
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     401 LHPLMARPVVPTRGRPLLLKRNVR YTHLTGTHVSTPAGPTYDLLFLGTADGWIHKAVVLG 460

Qy     451 DSSAHLVEEIQLFPDPEPVRNLQLAPTQGA VFGFSGGVWRVPRANCSVYESCVDCVLAR 510
      | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     461 -SGMHIEEIQVFREPQSDNLVISPMQHSLYVGAASGVLQFPPLSSCSRYQSCYDCILAR 519

Qy     511 DPHCAWDPE SRTCCL--LSAPNLNSWKQDMERGNPEWACASGPM SRSRLRPQSRPQIIKEVL 569
      | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     520 DPYCGWDSSIHACMVATTVANRTELIQDIERNR--GCEG---SRDAGP---PPPLKTRS 571

Qy     570 AVPNSILELPCPHLSALASYW-SHGPAAVPEASSTVYNGSLLLIVQDGV---GGLYQCW 625
      : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     572 VLRGDDVLLPCDQPSNLARALWLLNGSKSLSDGQDGYRVGV DGLLVTD TQLEHSGNYGCY 631

Qy     626 ATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQSYWPHFV 685
      | | | | : | | : | | | | | | | | | | | | | | | | | | | | | | | | |
Db     632 AEENGLRMLLASYSLTVRPATPAPAPQAPATP-----GAQLA-----HDM 671

Qy     686 TVTVLFALVLSGALIILVASPL-----RALRARGKV----- 716
      : | : | : | | : | | | | | | | | | | | | | | | | | | | | | | | | |
Db     672 RMFYVVAIAILGGLCLILASSLLYVACLKGGRRGRRRKYS LGRAGRAGGS AVQLQTVSGQ 731
```

Qy 717 -----QGCETLRPGEKAP 729
 || : ||| ||
 Db 732 CPGEEDGDDGEGTGGLESGCLQIIPGEGAP 762

RESULT 9

SM4G_HUMAN

ID SM4G_HUMAN STANDARD; PRT; 838 AA.
 AC Q9NTN9; Q9HCF3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Semaphorin 4G precursor.
 GN SEMA4G OR KIAA1619.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Heath P.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20450683; PubMed=10997877;
 RA Nagase T., Kikuno R., Nakayama M., Hirose M., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes.
 RT XVIII. The complete sequences of 100 new cDNA clones from brain which
 RT code for large proteins in vitro.";
 RL DNA Res. 7:273-281(2000).
 CC -!- FUNCTION: MAY PLAY A ROLE IN AXON GUIDANCE (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AL133215; -; NOT_ANNOTATED_CDS.
 DR EMBL; AB046839; BAB13445.1; ALT_INIT.
 DR Genew; HGNC:10735; SEMA4G.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.

DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Signal; Transmembrane; Immunoglobulin domain; Multigene family;
 KW Neurogenesis; Developmental protein; Glycoprotein.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 838 SEMAPHORIN 4G.
 FT DOMAIN 18 675 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 676 696 POTENTIAL.
 FT DOMAIN 697 838 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 56 489 SEMA.
 FT DOMAIN 507 558 PSI.
 FT DOMAIN 567 649 IG-LIKE C2-TYPE.
 FT DOMAIN 565 568 POLY-PRO.
 FT DOMAIN 763 774 POLY-PRO.
 FT DISULFID 584 632 BY SIMILARITY.
 FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 598 598 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 543 543 R -> RSQGS (IN REF. 2).
 SQ SEQUENCE 838 AA; 91496 MW; 9B281AEE8681F245 CRC64;

Query Match 23.8%; Score 958; DB 1; Length 838;
 Best Local Similarity 34.7%; Pred. No. 3.2e-69;
 Matches 259; Conservative 101; Mismatches 255; Indels 132; Gaps 27;

Qy 57 HQKG-LQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAF 115
 | | | | | : : | | | | | | | | | | | | | | : : |
 Db 48 HFKGQAQNYSTLLLEEASARLLVGARGALFSLSANDIGDGAHKE-IHWEASPEMQSKCHQ 106
 Qy 116 KKKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQ 175
 | | : : | : | | | | | | | | | | | : : : | | : | | :
 Db 107 KGKNNQTECFNHVRFLQRLNSTHLYACGTHAFQPLCAAID-AEAFTLPTSFE---EGKEK 162
 Qy 176 SPFDPAHKHTAVLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFV- 234
 | : | | | | : : | | | : | | | : | : : : | | : | | |
 Db 163 CPYDPARGFTGLIIDGGLYTATRYEF-RSIPDIRRSRPHSLRTEETPMHWL-NDAEEFVF 220
 Qy 235 -----AAIPSTQVVYFFFEETASE-----FDFFERLH-TSRVARVCKNDVGGEKLL 279
 : | : | | | | | : | | | | | : | | | | | : | : | : |
 Db 221 SVLVRESKASAVGDDDKVYFFTERATEEGSGSFTQSRSSHRVARVARVCKGDLGGKKIL 280
 Qy 280 QKKWTTFLKAQLLCTQPGQLPFNVIRHAVLLPADSPTAPHIYAVFT--SQWQVGGRSSA 337
 | | | | : | | | : | | : : | | | | : | | : | | : | |
 Db 281 QKKWTSFLKARLICHIP---LYETLRGVCSLDAETSSRTHFYAAFTLSTQWKT--LEASA 335
 Qy 338 VCAFSLLDIERVFKGKYKELNKETSRWTTYRGPETNPRPGSC-----SVGPSSDK---- 387
 : | : | : | | | | : | | | | | | | | | | : | :
 Db 336 ICRYDLAEIQAVFAGPYMEYQDGSRRWGRYEGGVPEPRPGSCITDSLRSQGYNSSQDLPS 395
 Qy 388 -ALTFMKDHFLLMDEQVV---GTPLLVKSVEYTRLAVETAQGLDGHSHLVMYLGTGTTGSL 443
 | | : | | | | | | | | : | | | | : : : : | | :
 Db 396 LVLDLVKLHPLMARPVVPTGRPLLLKRNIRYTHLTGTPVTTTTPAGPTYDLLFLGTADGWI 455
 Qy 444 HKAVVSGDSSAHLVEEIQLFDPPEFVRNLQLAPTQGAFFVGFSGGVWRVPRANCSVYESC 503

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      ||||| | | |::|| |:: | : | || :: | ::|| | | ::| ::|| | ||
Db      456 HKAVVLG-SGMHIIETQVFRESQSVENLVISLLQHSLYVGAPSGVIQLPLSSCSRYRSC 514
Qy      504 VDCVLARDPHCAWDPESSERTCCLLSA-PNLNSWKQDMERGNPEWACASGPMRSRLRPQSRP 562
      ||:|||||:| ||| : | : | : ||:|||| | | || | | |
Db      515 YDCILARDPYCGWDPGTHACAAATTIANRTALIQDIERNR--GCES---SRDTGP---P 566
Qy      563 QIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAVPEASSTVYNGSLLLIVQDGVGGL- 621
      :| : : ||| | || | : |||: | || ||
Db      567 PPLKTRSVLRGDDVLLPCDQPSNLARALW-----LLNGSMGL--SDGQGGYR 611
Qy      622 -----YQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKV 663
      | |:| ||| : || : : | | |: |
Db      612 VGVDGLLVTDAQPEHSGNYGCGYAEENGLRTL LASYSLTVRPATPAPAPKAPATP----- 665
Qy      664 PLTRVSGGAALAAQSYWPHFVTVTVL FALVLSGALIILVASPL----- 707
      || || | : : |: | | ::|| |
Db      666 -----GAQLAPD-----VRLLYVLAIAALGGLCLILASSLLYVACLREGRRGRRRK 711
Qy      708 ----RALRARGKVQGCETLR---PGEK 727
      || || | :|: |||:
Db      712 YSLGRASRAGGSAVQLQTVSGQCPGEE 738

```

RESULT 10

SM4F_HUMAN

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ID   SM4F_HUMAN          STANDARD;          PRT;    770 AA.
AC   O95754; Q9NS35;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Semaphorin 4F precursor (Semaphorin W) (Sema W) (Semaphorin M) (Sema
DE   M).
GN   SEMA4F OR SEMAW OR SEMAM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM SMALL).
RC   TISSUE=Brain;
RX   MEDLINE=99162633; PubMed=10051670;
RA   Encinas J.A., Kikuchi K., Chedotal A., de Castro F., Goodman C.S.,
RA   Kimura T.;
RT   "Cloning, expression, and genetic mapping of Sema W, a member of the
RT   semaphorin family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:2491-2496(1999).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM LONG).
RA   Chen F., Do A., Do T., Meisler M., Roe B.A.;
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM LONG).
RC   TISSUE=Amygdala;
RX   MEDLINE=21154917; PubMed=11230166;
RA   Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA   Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,

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RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
 RA Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
 RA Wambutt R., Korn B., Klein M., Poustka A.;
 RT "Towards a catalog of human genes and proteins: sequencing and
 RT analysis of 500 novel complete protein coding human cDNAs.";
 RL Genome Res. 11:422-435(2001).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 347-770 FROM N.A.
 RA Jang W., Spilson S.V., Hua A., Roe B., Meisler M.H.;
 RT "Large-scale comparative sequence analysis of human and mouse genomic
 RT DNA in the mnd2 region of mouse chromosome 6 reveals coding regions of
 RT three new genes.";
 RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Has growth cone collapse activity against retinal
 CC ganglion-cell axons (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=O95754-1; Sequence=Displayed;
 CC Name=Short;
 CC IsoId=O95754-2; Sequence=VSP_006043;
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -----
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CC -----

DR EMBL; AB022317; BAA75631.1; -.

DR EMBL; AC006544; -; NOT_ANNOTATED_CDS.

DR EMBL; AL136552; CAB66487.1; -.

DR EMBL; BC018361; AAH18361.1; -.

DR EMBL; AF053369; AAF80660.1; -.

DR Genew; HGNC:10734; SEMA4F.

DR MIM; 603706; -.

DR GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0005624; C:membrane fraction; TAS.

DR GO; GO:0007411; P:axon guidance; TAS.

DR GO; GO:0007267; P:cell-cell signaling; TAS.

DR GO; GO:0007399; P:neurogenesis; TAS.

DR InterPro; IPR003659; Plexin-like.

DR InterPro; IPR002165; Plexin_repeat.

DR InterPro; IPR001627; Sema.

DR Pfam; PF01437; PSI; 1.

DR Pfam; PF01403; Sema; 1.

DR SMART; SM00423; PSI; 1.

DR SMART; SM00630; Sema; 1.

KW Signal; Transmembrane; Immunoglobulin domain; Multigene family;

KW Neurogenesis; Developmental protein; Glycoprotein;

KW Alternative splicing.

FT	SIGNAL	1	34	POTENTIAL.
FT	CHAIN	35	770	SEMAPHORIN 4F.
FT	DOMAIN	35	659	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	660	680	POTENTIAL.
FT	DOMAIN	681	770	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	65	496	SEMA.
FT	DOMAIN	512	563	PSI.
FT	DOMAIN	580	635	IG-LIKE C2-TYPE.
FT	DISULFID	587	628	BY SIMILARITY.
FT	CARBOHYD	64	64	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	133	133	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	509	509	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSP LIC	120	274	Missing (in isoform Short).
FT				/FTId=VSP_006043.
FT	CONFLICT	533	533	S -> N (IN REF. 1).
SQ	SEQUENCE	770 AA;	83511 MW;	CFBB74B41DF0E9C8 CRC64;

Query Match 22.8%; Score 919.5; DB 1; Length 770;

Best Local Similarity 32.8%; Pred. No. 3.6e-66;

Matches 250; Conservative 109; Mismatches 309; Indels 95; Gaps 24;

Qy	19	FQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSEFFHQKGLQDFDTLLLSGDGNTLYV	78
		: : : : : : :	
Db	20	FPLLLLA VLSGPVSGRVPRSVPR TSLPISEAD SCLTRFAVPHTYNYSVLLVDPASHTLYV	79
Qy	79	GAREAILALDIQDPGV-PRLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVT	137
		: : : : : :: :	
Db	80	GARDTIFALS L PFSGERPR---RIDWMVPEAHRQNC R-KKGKKEDECHNFVQILA IANAS	135
Qy	138	HL YTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDP AHKHTAVLVDGMLYSGT	197
		: : : : : : : : :	
Db	136	HLLTCGTFAFD PKCGVIDVSRFQQV----ERLESGRGKCPFEPAQRSAAVMAGGVLYAAT	191
Qy	198	MN N FLGSEPI LMRTL G-SQPV LKTDN FLRWLHHDASFVAAIPSTQV-----VYFF	246

RA Halloran M.C., Severance S.M., Yee C.S., Gemza D.L., Kuwada J.Y.;
 RT "Molecular cloning and expression of two novel zebrafish
 RT semaphorins.";
 RL Mech. Dev. 76:165-168(1998).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -----
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 CC -----
 DR EMBL; AF073289; AAC72345.1; -.
 DR ZFIN; ZDB-GENE-990715-7; sema7.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Signal; Transmembrane; Immunoglobulin domain; Multigene family;
 KW Glycoprotein.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 766 SEMAPHORIN 27.
 FT DOMAIN 25 664 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 665 685 POTENTIAL.
 FT DOMAIN 686 766 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 53 483 SEMA.
 FT DOMAIN 501 552 PSI.
 FT DOMAIN 555 640 IG-LIKE C2-TYPE.
 FT DISULFID 577 623 BY SIMILARITY.
 FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 564 564 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 766 AA; 85617 MW; 0ACBC693FE7D830C CRC64;

Query Match 22.7%; Score 917; DB 1; Length 766;
 Best Local Similarity 34.1%; Pred. No. 5.8e-66;
 Matches 250; Conservative 126; Mismatches 258; Indels 100; Gaps 29;

QY 12 SLLGLFLFQLLQLLLPTTTAGGGGQ--GPMPRVRYAGDERRALSFFHQKGLQDFDTLLL 69
 ||| : :| : | ||| :|| | | :||| :||
 Db 3 SLLAVLC--VLYVWSPAMLTGGLGSTLDSLPRKTVPIGSNGGRL--FREEGIWNYTTMLL 58
 QY 70 SGDGNLTLYVGAREAILALDIQDPGVPRLNMI PWPASDRKKSECAFKKKSNETQCFNFIR 129

Db 59 RDDLNLLILGAREAIFALDLD--ITIKKAMLKWEVTRDQQNDCSNKGKDATNDCKNYIR 116
 Qy 130 VLVSYNVTHLYTCGTFAFSPACTFIELQDSYL-LPISEDKVMEGKGQSPFDPAHKHTAVL 188
 Db 117 ILHKKNDGRMYVCGTKAFNPTCGYLSYADGKLTLEILQE---DTKGKCPDFPFQRYTSAM 173
 Qy 189 VDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFV--AAIPSTQ----- 241
 Db 174 VDGAYYSATSMNFRGSEPVMRS--TEESIRTEFTSTWL-SEPNFIHMAHIPEGQSNPDG 230
 Qy 242 ---VVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPG- 297
 Db 231 DDDKIYLFSETAVEYESYTKVDVSRVARVCKGDLGGQRTLQKKWTSFLKARLDCQVPNT 290
 Qy 298 QLPFNVIRHAVLLPADSPTAPHIYAVFTSQVQVGTRSSAVCAFSLLDIERVF-KGKYK- 355
 Db 291 NLPL-LVQDVHLCPPDWTTCVIFYAVFTP--QSDSSQYSAVCSYKIEDIKTVFSKGKFA 347
 Qy 356 ELNKETS--RWTTYRGPETNPRPGSC-----SVGPS---SDKALTFMKDHFMLDEQV 402
 Db 348 PFNVETSFVKWVMYSGELPDPRPGACIDNHAREKGITKSLELPDKTLQFVKDKPLMDQAV 407
 Qy 403 VG-TPLLVKSGVEYTRLAVETAQGLDGHSHLVMYLGTGSLHKAVVSGDSSAHLVEEIQ 461
 Db 408 TAEQPLLVKRGAAFTTRIVTTATALNGTSHQVMFIGTKSGSVLKA-VNYNGEMVIMEEIQ 466
 Qy 462 LFPDPEPVRNLQ LAPTQGA VFVGSGGVWRVPRANCSVYESCVDCVLARDPHCAWD PESR 521
 Db 467 LFDPEPIKILRLSSSKQLYVGSEVGVVQLSISECGRYQTCLDCVLARDPHCGWDLDE 526
 Qy 522 TCCLLSA---PNLNSWKQDMERGNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILEL 578
 Db 527 HCATINSIHRTRSSTVIQSLNDGDASQCPAIG-----VSKP---VNISFYHGNTVKL 575
 Qy 579 PCPHLSALASYWWSHGPAAVPEASS-----TVYNGSLLLIVQDGVGGLYQCWATENG 630
 Db 576 GCQPYSNLAQVKWQFNGEPIKPSNTIQILSDGLMIFNASL-----DATGYTCSSET- 628
 Qy 631 FSYPVISYWVDS---QDQTLALDPELAGIPREHVKVPLTRVSG-GAALAAQQSYWPHFVT 686
 Db 629 -----VSQRKYQTQHVAID-----VKMWSESGTTASLHHVKEKERTIVA 667
 Qy 687 VTVLFALVLSGALI 700
 Db 668 MVVILSLVLAALLI 681

RESULT 12

SM4F_MOUSE

ID SM4F_MOUSE STANDARD; PRT; 777 AA.
 AC Q9Z123; Q9R1Y1;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Semaphorin 4F precursor (Semaphorin W) (Sema W).
 GN SEMA4F OR SEMAW.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c, and 129/SvJ; TISSUE=Brain;
 RX MEDLINE=99162633; PubMed=10051670;
 RA Encinas J.A., Kikuchi K., Chedotal A., de Castro F., Goodman C.S.,
 RA Kimura T.;
 RT "Cloning, expression, and genetic mapping of Sema W, a member of the
 RT semaphorin family."
 RL Proc. Natl. Acad. Sci. U.S.A. 96:2491-2496(1999).
 CC -!- FUNCTION: Has growth cone collapse activity against retinal
 CC ganglion-cell axons (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB021291; BAA75630.1; -.
 DR EMBL; AB022316; BAA75634.1; -.
 DR EMBL; AB022311; BAA75634.1; JOINED.
 DR EMBL; AB022312; BAA75634.1; JOINED.
 DR EMBL; AB022313; BAA75634.1; JOINED.
 DR EMBL; AB022314; BAA75634.1; JOINED.
 DR EMBL; AB022315; BAA75634.1; JOINED.
 DR MGD; MGI:1340055; Sema4f.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 KW Signal; Transmembrane; Immunoglobulin domain; Multigene family;
 KW Neurogenesis; Developmental protein; Glycoprotein.
 FT SIGNAL 1 40 POTENTIAL.
 FT CHAIN 41 777 SEMAPHORIN 4F.
 FT DOMAIN 41 667 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 668 688 POTENTIAL.
 FT DOMAIN 689 777 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 71 502 SEMA.
 FT DOMAIN 518 569 PSI.
 FT DOMAIN 586 641 IG-LIKE C2-TYPE.
 FT DISULFID 593 634 BY SIMILARITY.
 FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 515 515 N-LINKED (GLCNAC. . .) (POTENTIAL).

```

FT    VARIANT      490      490      P -> T (IN STRAIN 129/SVJ).
FT    VARIANT      659      659      S -> A (IN STRAIN 129/SVJ).
SQ    SEQUENCE     777 AA;  84501 MW;  B63F853355856924 CRC64;

```

Qy	21	LLQLLLPTTTTAGGGGQGP--MPRVRYYAGDERRALSFHQKGLQDFDFTLLLSGDGNTLYV	78
Db	26	LLLLLLAMLSAPVCGRVPRSPRTSLPISEADSYLTRFAAPHTYNYSALLVDPASHTLYV	85
Qy	79	GAREAILALDIQDPG--VPRLNMI PWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVT	137
Db	86	GARDSIFALTLPFSGEKPR---RIDWMVPETHRQNCR-KKGKKEDECHNFIQILAIANAS	141
Qy	138	HLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDPAHKHTAVLVDMGLYSGT	197
Db	142	HLLTCGTFAFDPKCGVIDVSSFQQV----ERLESGRGKCPFEPAQRSAAVMAGGVLYTAT	197
Qy	198	MNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAI-----PSTQVVYFF	246
Db	198	VKNFLGTEPIISRAGRAEDWIRTETLSSWLNAPA-FVAAMVLSPAEWGDEDGDDEIFFF	256
Qy	247	FEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQP--GQLPFNVI	304
Db	257	FTETSRVLDSYERIKVPRVARVCAGDLGGRKTLQQRWTTFLKADLLCPGPEHGRASGVLO	316
Qy	305	RHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRW	364
Db	317	DMTELRPQPGAGTPLFYGIFSSQWE--GAAISAVCAFRPQDIRAVLNGPFRELKHCNRRG	374
Qy	365	TTYRGPET-NPRPGSC-----SVGPS---SDKALTFMKDHFLLMDEQVV---GTPLL	409
Db	375	LPVMDNEVPQPRPGECITNNMKFQQFGSSLSLPDRVLTFRDHPLMDRPVFPADGRPLL	434
Qy	410	KSGVEYTRLAVETAQGLDGHSHLVMYLGTTTGS LHKAVVSGDSSAHLVEEIQLFDPPEPV	469
Db	435	TTDTAYLRVVAHRVTSLSGKEYDVLYLGTEDEGHLHRAVRIG-AQLSVLEDLALFPEPQPV	493
Qy	470	RNLQLAPTQGAVFVGFSGGVWRVPRANCSVYESCVCVLARDPHCAWDPESTRCCLLSAP	529
Db	494	ESMKL--YHDWLLVGSHTTEVTQVNTSNCGRQLQSCSECILAQDPVCAWS-FRLDACVAHAG	550
Qy	530	NLNSWKQDMERGNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILELPCPHLSALASY	589
Db	551	EHRGMVQDIESADVSSLCPK-----EPGEHPVVFEVPVATVGHVV-LPCSPSSAWASC	602
Qy	590	YWSHGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLAL	649
Db	603	VW-HQPSGV--TSLTPRRDGLEVVVTPGAMGAYACECQEGGAARVVAAY-----SLVW	652
Qy	650	DPELAGIPREHVKVPLTRVSGGAALAAQQSYWPHFVTVTVLFLVLSGALIILVAS----	705
Db	653	GSQRGPSNRAHTVV-----GAGLVG-----FFLGVLAAASLTLLLIIGRRQQ	692
Qy	706	--PLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECR	743

Db

693 RRRQRELLARDKVGLDLGAPPSGTTSYSQDPPSPSPEDER 732

RESULT 13

SM4F_RAT

ID SM4F_RAT STANDARD; PRT; 776 AA.
AC Q9Z143;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Semaphorin 4F precursor (Semaphorin W) (Sema W).
GN SEMA4F.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=99162633; PubMed=10051670;
RA Encinas J.A., Kikuchi K., Chedotal A., de Castro F., Goodman C.S.,
RA Kimura T.;
RT "Cloning, expression, and genetic mapping of Sema W, a member of the
RT semaphorin family."
RL Proc. Natl. Acad. Sci. U.S.A. 96:2491-2496(1999).
CC -!- FUNCTION: Has growth cone collapse activity against retinal
CC ganglion-cell axons.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED AT LOW LEVELS IN THE DEVELOPING
CC EMBRYO. EXPRESSED AT HIGH LEVELS IN THE ADULT CENTRAL NERVOUS
CC SYSTEM AND LUNG.
CC -!- SIMILARITY: Belongs to the semaphorin family.
CC -!- SIMILARITY: Contains 1 Sema domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB002563; BAA75629.1; -.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR InterPro; IPR001627; Sema.
DR Pfam; PF01437; PSI; 1.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
KW Signal; Transmembrane; Immunoglobulin domain; Multigene family;
KW Neurogenesis; Developmental protein; Glycoprotein.
FT SIGNAL 1 39 POTENTIAL.
FT CHAIN 40 776 SEMAPHORIN 4F.
FT DOMAIN 40 665 EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	666	686	POTENTIAL.
FT	DOMAIN	687	776	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	70	501	SEMA.
FT	DOMAIN	517	568	PSI.
FT	DOMAIN	585	640	IG-LIKE C2-TYPE.
FT	DISULFID	592	633	BY SIMILARITY.
FT	CARBOHYD	69	69	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	138	138	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	514	514	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	776 AA;	84298 MW;	20763182CC6C93CA CRC64;

Query Match 22.4%; Score 901.5; DB 1; Length 776;
 Best Local Similarity 33.0%; Pred. No. 1.1e-64;
 Matches 255; Conservative 108; Mismatches 308; Indels 101; Gaps 27;

QY	10	PWSLLGLFLFQLLQLLLPTTTAGGGGQGP--MPRVRYAGDERRALSFFHQKGLQDFDTL	67
		: : : : :	
Db	23	PLSLL-----LLLAISAPVCGRVPRSVPTSLPISEADSYLTFRAASHTYNYSAL	73
QY	68	LLSGDGNTLYVGAREAILALDIQDPGV-PRLKNMIPWPASDRKKSECAFKKKSNETQCFN	126
		: : : : : : :	
Db	74	LVDPASHTLYVGARDSIFALTLPFSGERPR---RIDWMVPETHRQNCR-KKGKKEDECHN	129
QY	127	FIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMGKGQSPFDPAHKHTA	186
		: : : : : : : :	
Db	130	FIQILAIVNASHLLTCGTFAFDPKCGVIDVSSFQQV----ERLESGRGKCPFEPAQRSAA	185
QY	187	VLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAI-----	237
		: : : : : : : : : : : : :	
Db	186	VMAGGVLYTATVKNFLGTEPIISRAGRAEDWIRTETLSSWLNAPA-FVAAMVLSPAEWG	244
QY	238	--PSTQVVYFFFEETASEFDDFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQ	295
		: : : : : :	
Db	245	DEDGDDEIFFFFETETSRVLDSYERIKVPRVARVCAGDLGGRKTLQQRWTTFLKADLLCPG	304
QY	296	P--GQLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGK	353
		: : : : :	
Db	305	PEHGRASGVLQAMAELRPQPGAGTPIFYGIFSSQWE--GAAISAVCAFRPQDIRAVLNGP	362
QY	354	YKELNKETSRWTTYRGPET-NPRPGSC-----SVGPS---SDKALTFMKDHFILMDEQ	401
		: : : : :	
Db	363	FRELKHCNRLPVMNEVPQPRPEGECIANNMKLQQFGSSLSLPDRVLTFFIRDHPLMDRP	422
QY	402	VV---GTPLLKSGVEYTRLAVETAQGLDGHSHLVMYLGTTGSLHKAVVSGDSSAHLVE	458
		: : : : : : :	
Db	423	VFPADGRPLLVTDTAYLRVVAHRVTSLSGKEYDVLYLGTEDGHLHRAVRIG-AQLSVLE	481
QY	459	EIQLFDPPEPVRNLQLAPTQGAVFVGFSGGVWRVPRANCSVYESCVDCVLARDPHCAWDP	518
		: : : : : : : : : : :	
Db	482	DLALFPEPQPVESMKL--YHDWLLVGSHTEVTQVNTSNCGRLQSCSECILAQDPVCAWS-	538
QY	519	ESRTCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRPQSRPQIIKEVLAVPNSILEL	578
		: : : : : : : :	
Db	539	FRLDACVAHAGEHRGMVQDIESADVSSSLCPK-----EPGEHPVVFEVPVATVGHVV-L	590
QY	579	PCPHLSALASYWSHGPAAVPEASSTVYNGSLLLVQDGVGGGLYQCWATENGFSYPVISY	638
		: : : : :	

```

Db      591 PCSPSSAWASCVW-HQPSGV--TALTFRRDGLEVVVTPGAMGAYACECQEGGAARVVAAY 647
QY      639 WVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWPHFVTVTVLFAL-VLSG 697
          :| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      648 -----SLVWGSQRGPSNRAHTVV-----GAGL-----VGFLLGVLAA 679
QY      698 ALIILVAS-----PLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECR 743
          :| :| : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      680 SLTLLLLIGRRQQRRRQRELLARDKVGLDLGAPPSGTTSYSQDPPSPSPEDER 731

```

RESULT 14

SZ1A_BRARE

```

ID      SZ1A_BRARE      STANDARD;      PRT;      860 AA.
AC      Q9W7J1;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Semaphorin Z1A precursor (Semaphorin 1A) (Sema-Z1A).
GN      SEMAZ1A OR SEMA3AA.
OS      Brachydanio rerio (Zebrafish) (Danio rerio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Danio.
OX      NCBI_TaxID=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RX      MEDLINE=99313409; PubMed=10386838;
RA      Yee C.S., Chandrasekhar A., Halloran M.C., Shoji W., Warren J.T.,
RA      Kuwada J.Y.;
RT      "Molecular cloning, expression, and activity of zebrafish semaphorin
RT      Z1a.";
RL      Brain Res. Bull. 48:581-593(1999).
CC      -!- FUNCTION: MAY INFLUENCE OUTGROWTH BY A VARIETY OF GROWTH CONES
CC      INCLUDING THOSE OF THE POSTERIOR LATERAL LINE GANGLION.
CC      -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC      -!- DEVELOPMENTAL STAGE: EXPRESSED IN HIGHLY SPECIFIC PATTERNS WITHIN
CC      THE DEVELOPING EMBRYO.
CC      -!- SIMILARITY: Belongs to the semaphorin family.
CC      -!- SIMILARITY: Contains 1 Sema domain.
CC      -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF086761; AAD43964.1; -.
DR      ZFIN; ZDB-GENE-991209-3; sema3aa.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003599; Ig.
DR      InterPro; IPR003659; Plexin-like.
DR      InterPro; IPR001627; Sema.

```

DR Pfam; PF00047; ig; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Signal; Immunoglobulin domain; Multigene family; Neurogenesis;
 KW Developmental protein; Glycoprotein.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 860 SEMAPHORIN Z1A.
 FT DOMAIN 241 539 SEMA.
 FT DOMAIN 579 668 IG-LIKE C2-TYPE.
 FT DOMAIN 722 858 ARG/LYS-RICH (BASIC).
 FT DISULFID 652 717 BY SIMILARITY.
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 593 593 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 860 AA; 97263 MW; 5FD4C12194F5165C CRC64;

Query Match 21.8%; Score 880.5; DB 1; Length 860;
 Best Local Similarity 29.8%; Pred. No. 6.1e-63;
 Matches 239; Conservative 139; Mismatches 322; Indels 103; Gaps 25;

QY 13 LLGLFLFQLLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQD---FDTLLL 69
 |:|:| | : | | : :|:| : : : | | : :| | :
 Db 4 LVGIFLL-LCGVALPGRVAPQHTKENVPRLKLSYNEMLSSNLVFTFTGLANSSGYDTFLM 62
 QY 70 SGDGNLTLYVGAREAILALDIQDPGVPRLNMI PWPASDRKKSECAFKKKSNETQCFNFIR 129
 |: | | | : : : | : : : | | | : |: | | : | | | :
 Db 63 DGERGRLLVGAEDHVF SFDLVN--INRDVKQIAWPATPSKRDECKWAGKDLRKDCSNFVR 120
 QY 130 VLVSYNVTHLYTCGTF AFSPACTFIEL---QDSYLLPISEDKVMGKGQSPFDP AHKHTA 186
 || ||| ||:| ||| || | |:|:| : : : : |:|:|:| | : :
 Db 121 VLQSYNQTHIYICGTGAFHPICSFLEMGKRAEDNIFRLDANYFENGGRGKSPYDPKMQSSS 180
 QY 187 VLVDGMLYSGTMNFLGSEPILMRTLGSQPVLKTDNF-LRWLHHDASFV-----AAIP 238
 |:|:| | | | | : |:| : : | | | | : |:| | | | : |
 Db 181 LLLDGELYSGTSADFMGRDFAIFRTLGSHPHPIRTEQHD SRWL-NEPRFLGIHLIPESDNP 239
 QY 239 STQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPG- 297
 : : | |:| | : : : | |: : :| |:| : | | | | | |:| |
 Db 240 EDDKIFLFFKENAMDGEHTGKATISRIGQLCKNDMGHRSIVNKWTTFLKAKLTCSVPGL 299
 QY 298 ---QLPFNVIRHAVLLPADSPTAPHIYAVFTSQWQVGGRSSAVCAFSLLDIERVFKGKY 354
 |: : : |:| | | | | | | : : | |:| |:| :| | | | |
 Db 300 NGIDTHFDELQDVFLMSAKDPKNPVIYAVFTTSSNI--FRGSAICMYSMADIRRVFLGPY 357
 QY 355 KELNKETSRWTTYRG PETNPRPGSC-----SVGPSSDKALTFMKDHF LMD EQVV-- 403
 : :| : :| | | |:| | | :| :| :| | |
 Db 358 AHRDGP NYQWVPFQGRVPYPRPGT CPSKTFGGFDSTKDL PDDVITFARLHPAMYNPVQPM 417
 QY 404 -GTPLLVKSGVEY--TRLAVETAQGLDGHSHLV MYLGTTTGS LHKAVVSGDSSAH----- 455
 | |:|:|:| | | |:| |: : | | : |:|:| | |:| | | |
 Db 418 G GKPIVVRTNVEYQFTQLVVDRVEAEDG-QYDVMFIGTDLGTVLKVVTIPRESWHDLEEV 476
 QY 456 LVEEIQLFDPPEPVRNLQLAPTQGAVFVGFSGGVWRVPRANCSVY-ESCVCV LARDPHC 514
 : |:|:| :| :| : :|:| | : :| | : :| | | | :|

Db 477 VLEEMTVFREPTPITAMELSTKQQQLYLGSDLGISQMP LHRCEVYGKACAECC LARDPYC 536

QY 515 AWD PESRTCCLLSAPNL--NSWKQDMERGNPEWACASGPM SRS LRPQSRPQIIKEVLAVP 572
 ||| | | | : : || : | : | : : | |

Db 537 AWD---GTECSRYFPTAKRRTRRQDIRNGDPLSQCS DLHHND DLEGYSSVE-ERSVYGVE 592

QY 573 NSILELPCPHLSALASYYS-----HGPAAVPEASSTVYNGS LLLIVQDGVGGLYQC 624
 || : | | | | | : | | | | : : | : : |

Db 593 NSSMFLECSPKSQRALIYWQLQKPNDERKHEIVIDERLSL TGQGLLIRSLTQADSGVFLC 652

QY 625 WATENGFSYPVISYWVDSQDQTLALDPELAGIPREHV KVP LTRV-SGGAALAAQQSYW-- 681
 | : || | : | | | : | | : | : |

Db 653 HAVEHGFIQPLRRI-----NLQVIPSQRVGELL L RAGTNDKDPAPKHLWYR 699

QY 682 -----PHFVTVTVL FALVL SGALIILVASPLRALRARGKVQGCETLRPG-----E 726
 | : | : | : | : | | : | |

Db 700 DFMSLLEHPDLNSVDEF CERIWK-----REKKPKGK--KAPKVNPGTGVS IKNE 746

QY 727 KAPLSREQHLQSPKECRTSASDV 749
 | | : | | : | : | |

Db 747 KTPQT TAQSLQNPTQRAQNAPKV 769

RESULT 15

SM3F_MOUSE

ID SM3F_MOUSE STANDARD; PRT; 785 AA.

AC O88632; O88633;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Semaphorin 3F precursor (Semaphorin IV) (Sema IV).

GN SEMA3F.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS A AND B).

RX MEDLINE=99090943; PubMed=9875739;

RA Eckhardt F., Meyerhans A.;

RT "Cloning and expression pattern of a murine semaphorin homologous to

RT H-sema IV.";

RL NeuroReport 9:3975-3979(1998).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM A).

RC STRAIN=FVB/N; TISSUE=Colon;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=B;
 CC IsoId=O88632-1; Sequence=Displayed;
 CC Name=A;
 CC IsoId=O88632-2; Sequence=VSP_006042;
 CC -!- TISSUE SPECIFICITY: Expressed ubiquitously in adulthood. During
 CC embryogenesis, expressed in subregions of the central nervous
 CC system and various other tissues like skin, kidney, lung and
 CC intestine.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL; AF080090; AAC28108.1; -.
 DR EMBL; AF080091; AAC28109.1; -.
 DR EMBL; BC010976; AAH10976.1; -.
 DR MGD; MGI:1096347; Sema3f.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF00047; ig; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00408; IGc2; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Signal; Immunoglobulin domain; Multigene family; Glycoprotein;
 KW Alternative splicing.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 785 SEMAPHORIN 3F.
 FT DOMAIN 272 569 SEMA.
 FT DOMAIN 605 695 IG-LIKE C2-TYPE.
 FT DOMAIN 758 779 ARG/LYS-RICH (BASIC).
 FT DOMAIN 715 718 POLY-PRO.
 FT DISULFID 678 746 BY SIMILARITY.
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 126 126 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 153 183 Missing (in isoform A).
 FT /FTId=VSP_006042.
 SQ SEQUENCE 785 AA; 88493 MW; 89DBA7A08D02A72E CRC64;

Query Match 20.9%; Score 841; DB 1; Length 785;
 Best Local Similarity 29.6%; Pred. No. 8.3e-60;
 Matches 249; Conservative 120; Mismatches 289; Indels 182; Gaps 35;

Qy 11 WS--LLGLFLFQLLQLLLPTTTAGGGGQGMPRVRYAGDERRALSFFHQK----- 59
 | : | | : : | | | | | | | | | | | | | | | | | |
 Db 9 WASLLTGAWPATPIQDQLPAT-----PRVR-----LSFKELKATGTAHFFN 49

Qy 60 ---GLQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFK 116
 | : | | | : : | | : : | | : : | : | : | | : : | |
 Db 50 FLLNTTDYRILLKDEDHDMYVGS KDYVLSLDLHD--INREPLIIHWAASPQRIEECILS 107

Qy 117 KKSNETQCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIEL----- 156
 | : | | : : | | | | | | | | : : | | : :
 Db 108 GKDGNGECGNFVRLIQPNRTHLYVCGTGAYNPMCTYVNRGRRAQALPWTQM QVVVRGRGS 167

Qy 157 -----QDSYLLPISEDKVMEGKGQSPFDPAHKHTAVLVDGMLYSGTMNNFL 202
 : | : : : | | : | | : | : : | | : | :
 Db 168 RATDGADRPTPTAPRQDYIFYLEPEKLESGKGKCPYDPKLD TASALINEELYAGVYIDFM 227

Qy 203 GSEPILMRTLGSQPVLKTDNF-LRWLHHDASFVAA--IPST-----QVVYFFFEETASEF 254
 | : : | | | | : : | | : | | : | | : : | | | | : : |
 Db 228 GTDAAI FRTL GKQTAMRTDQYNSRWL-NDPSFIHAELIPDSAERNDDKLYFFFRERSAEA 286

Qy 255 DFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPG----QLPFNVIRHAVLL 310
 : : : | : | | | | | | | | | | | | : | : : :
 Db 287 PQNPAVY-ARIGRICLNDGGHCCLVNKWSTFLKARLVCSVPGEDGIETHFDELQDVFVQ 345

Qy 311 PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTTYRGP 370
 | | | | | | | | | | | | : : | | | : : | : |
 Db 346 QTQDIRNPVIYAVFTSSGSV--FRGSAVCVYSMADIRMFVNGPF AHKEGPNYQWMPFSGK 403

Qy 371 ETNPRPGSCSVG---PS-----SDKALTFMKDHF LMDQV---GTPLLVKSGVEY-- 415
 | | | : | | | | | : : | | : | | : | | : | : |
 Db 404 MPYPRPGTCPGGTFTPSMKSTKDY PDEVINFMRTHPLMYQAVYPLQRRPLVVRTGAPYRL 463

Qy 416 TRLAVETAQGLDGHSHLVMYLGTTTGS LHKAV--SGDSSAH--LVEEIQLFPDPEPVRN 471
 | : | : | | : : | | : : | : | : | : : | : | : |
 Db 464 TTVAVDQVDAADGR-YEVLFLGTDRGTVQKVI VLPKDDQEVEELMLEEVEVFKEPAPVKT 522

Qy 472 LQLAPTQGA VFGVFGSGGVWRVPRANCSVY-ESCVD CVLARDPHCAWDPE SRTCCLLSAPN 530
 : : : : : | : | : | : | : | | | | : | : | :
 Db 523 MTISSKRQQLYVASAVGVTHLSLHRCQAYGAACADCC LARDPYCAWD--GQAC SRYTASS 580

Qy 531 -LNSWKQDMERGNPEWACASGPM SRSRLRPQSRPQIIKEV-LAVPNSILELPCPHLSALAS 588
 | : | : | | | : : : : | | | | | : | :
 Db 581 KRRSRRQDVRHGNPIRQC-----RGFNSNANKNAVESVQYGVAGSAAFLECQPRSPQAT 634

Qy 589 YYW--SHGPA-----AVPEASSTVYNGSLLLIVQDGVGGLYQCWATENGFSYPV--ISY 638
 | : | : : | | : | | | | | | : | :
 Db 635 VKWLFQRDP SDRRREIRAEDRFLRTEQGLLLRALQLGDRGLYSCTATENNFKHIVTRVQL 694

QY	639	WVDSQDQT-LALDPELAGIPREHVKVPLTRVSGG-----AALAAQ-----	QS	679
		: :		
Db	695	HVLGRDAVHAALFPPLA-----VSVPPPPGTGPPTPPYQELAQLLAQPEVGLIHQYCQG		748
QY	680	YWPHFVTVTVLFLVLGALIIILVASPLRALRARGKVQGCETLRPGE-----KAPLSREQH		735
		: :		
Db	749	YWRH-----VPPSPREAPGA-----LRPPELQDQKKPRNRRHH		781

Search completed: May 5, 2004, 17:29:11
Job time : 20 secs